

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p1ue\_p2n model

Run on: March 22, 2005, 05:20:43 | Search time 564 Seconds  
(without alignments)  
2248.292 Million cell updates/sec

Title: US-09-525-867-1  
Perfect score: 1118  
Sequence: 1 MAVLSAPQGLKGFRLGRSS.....ILQQRKIKRRRLQIYWR 213

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5544816 seqs, 2976611598 residues  
Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPFO.epool/h/US09525867/rnatc\_21032005\_055412\_1219/app\_query.fasta\_1.391  
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -WATTS=1locum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.\*  
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20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1118	100.0	772	US-10-037-270-670	Sequence 670, App
2	1118	100.0	772	US-10-117-722-670	Sequence 670, App
3	965	86.3	2818	US-10-104-047-625	Sequence 625, App
4	891.5	79.7	3089	US-10-104-047-914	Sequence 914, App
5	863	77.2	3050	US-10-104-047-262	Sequence 262, App
6	743	66.5	797	US-10-767-701-19893	Sequence 19893, A
7	740.5	66.2	1092	US-10-767-701-14502	Sequence 14502, A
8	737.5	66.0	886	US-10-425-114-16284	Sequence 16284, A
9	737.5	66.0	949	US-10-425-114-6711	Sequence 6711, App
10	737.5	66.0	1394	US-10-425-115-3877	Sequence 3877, App
11	735.5	65.8	1840	US-10-425-115-3875	Sequence 3875, App
12	731.5	65.4	753	US-10-320-797-2049	Sequence 2049, App
13	729	65.2	1356	US-10-424-599-6216	Sequence 6216, App
14	726.5	65.0	863	US-10-425-114-36399	Sequence 36399, A
15	725	64.8	1532	US-10-424-599-6217	Sequence 6217, App
16	723.5	64.7	1142	US-10-437-963-92496	Sequence 92496, A
17	702	62.4	735	US-10-128-714-7030	Sequence 7030, App
18	698	62.4	672	US-10-032-585-6755	Sequence 6755, App
19	676	60.5	466	US-10-152-319A-195	Sequence 195, App
20	670.5	60.0	570	US-10-128-714-2030	Sequence 2030, App
21	654	58.5	2731748	US-10-297-465A-1	Sequence 1, Appl
22	638.5	57.1	596	US-10-128-714-1030	Sequence 1030, App
23	638.5	57.1	873	US-10-128-714-6030	Sequence 6030, App
24	638.5	57.1	2596	US-10-128-714-30	Sequence 30, Appl
25	638.5	57.1	2873	US-10-128-714-5030	Sequence 5030, App
26	619	55.4	966	US-10-320-797-1049	Sequence 1049, App
27	619	55.4	2420	US-10-320-797-49	Sequence 49, Appl
28	618	55.3	344	US-10-775-169-55	Sequence 55, Appl
29	496.5	44.4	480	US-10-335-977-1662	Sequence 1662, App
30	458.5	41.0	9025608	US-10-156-761-1	Sequence 1, Appl
31	453.5	40.6	609	US-10-156-761-4866	Sequence 4866, Appl
32	441	39.4	274	US-10-425-115-158531	Sequence 158531, App
33	441	39.4	552	US-10-156-761-4822	Sequence 4822, App
34	433.5	38.8	3148	US-10-424-599-30088	Sequence 30088, A
35	431.5	38.6	58909	US-10-672-787-30	Sequence 30, Appl
36	429.5	38.4	4352	US-10-425-115-37889	Sequence 37889, A
37	428	38.3	640681	US-09-790-988-1	Sequence 1, Appl
38	418	37.4	446	US-09-991-936-1794	Sequence 1794, App
39	411	36.8	789	US-09-759-163-32	Sequence 32, Appl
40	411	36.8	789	US-09-780-669-32	Sequence 32, Appl
41	411	36.8	789	US-09-030-606-32	Sequence 32, Appl
42	411	36.8	789	US-09-822-827-32	Sequence 32, Appl
43	411	36.8	789	US-09-115-453-32	Sequence 32, Appl
44	411	36.8	789	US-09-232-880-32	Sequence 32, Appl
45	411	36.8	789	US-09-895-793-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-10-037-270-670 Application US/10037270

Sequence 670, Publication No. US20030104529A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyun

APPLICANT: Chen, Ruihong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aihong J.

APPLICANT: Yang, Yonghong

APPLICANT: Zhang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yunqing

APPLICANT: Wang, Duntui

APPLICANT: Wang, Zhiwei

APPLICANT: Tillinghast, John  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and  
FILE REFERENCE: 784CIP28  
CURRENT APPLICATION NUMBER: US/10/037,270  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1104  
SOFTWARE: pc\_FL\_genes Version 1.0  
SEQ ID NO 670  
LENGTH: 772  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (24) .. (665)  
US-10-037-270-670

Alignment Scores:  
Pred. No.: 7,686-135 Length: 772  
Score: 1118.00 Matches: 213  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-525-867-1 (1-213) x US-10-037-270-670 (1-772)

QY 1 MetAlaValIleuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20  
DB 24 ATGGCGGTGCTGCTCACTGCTGCTGCGCGGCTTCGGATCTTGCTGCTGCTCCAGC 83  
QY 21 ValGlyProAlaValAlaGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40  
DB 84 GTGGGCGCGCTGTGCAGGACGACGAGGTGTCATCAGAGGTGGCCACGAGTGGCCCAAGC 143  
QY 41 SerThrGlnProAlaLeuProIleValAlaArgAlaValAlaProIleProSerSerArgGly 60  
DB 144 AGCACCCAGCTGCTGCTGCCAAGGCGAAGCGGTGCTCCCAAAACCCAGCAGCCGGGCG 203  
QY 61 GluTyrValAlaAlaLysLeuAspAspLeuValAsnTPAlaArgSerSerLeuTyr 80  
DB 204 GAGTATGTGTGGCCAAAGCTGGATGACCTGTCACACTGGCCCCCGAGTCTCTGTGG 263  
QY 81 PrometThrPheGlyLeuAlaCysGlyAlaValGluMetMetHisMetAlaAlaProArg 100  
DB 264 CCCATGACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323  
QY 101 TyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMet 120  
DB 324 TACGACATGAGCACCGCTTTGGCGTGTCTTCGCCGCCAGCCCGGCCAGTCCGACGTCTAG 383  
QY 121 IleValAlaGlyThrIleuThrAsnLysMetAlaProAlaLeuArgLysValTyrAspGln 140  
DB 384 ATCTGGCCCGGACACCTCACCAACAGATGAGCCCGCTGCGCAAGGTCTACGACGAC 443  
QY 141 MetProGlnProArgTyrValAlaSerMetGlySerCysAlaAsnGlyGlyTyrTyr 160  
DB 444 ATGCGGAGCGCGCTACGTGTCTCATGTGGAGCTGGCCCAAGGAGGACCTAC 503  
QY 161 HisTyrSerTyrSerValAlaArgGlyCysAspArgIleValProValAspIleTyrTyr 180  
DB 504 CACTATCTCACTGTGTGTGAGAGGGCTGACCGCATCGTGGCCGTGACATCTACATC 563  
QY 181 ProGlyCysProProThrAlaGlnAlaLeuIleuTyrGlyIleLeuGlnLeuGlnArgLys 200  
DB 564 CCAGGCTGCCACCTACGCGCGAGGCCCTGCTCTACGCGCATCTTCAGCTGACGAGGAG 623  
QY 201 IleLysArgGlnArgArgLeuGlnIleTyrTyrArg 213

DB 624 ATCAAGCGGAGCGAGGCTGCAAGATCTGTGACCGCAG 662

RESULT 2

US-10-117-722-670  
Sequence 670, Application US/10117722  
Publication No. US20030219744A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and  
FILE REFERENCE: 784CIP28CIP  
CURRENT APPLICATION NUMBER: US/10/117,722  
PRIOR FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: 09/620,312  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1104  
SOFTWARE: pc\_FL\_genes Version 1.0  
SEQ ID NO 670  
LENGTH: 772  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (24) .. (665)  
US-10-117-722-670

Alignment Scores:  
Pred. No.: 7,686-135 Length: 772  
Score: 1118.00 Matches: 213  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

US-09-525-867-1 (1-213) x US-10-117-722-670 (1-772)

QY 1 MetAlaValIleuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20  
DB 24 ATGGCGGTGCTGCTCACTGCTGCTGCGCGGCTTCGGATCTTGCTGCTGCTCCAGC 83  
QY 21 ValGlyProAlaValAlaGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40  
DB 84 GTGGGCGCGCTGTGCAGGACGACGAGGTGTCATCAGAGGTGGCCACGAGTGGCCCAAGC 143  
QY 41 SerThrGlnProAlaLeuProIleValAlaArgAlaValAlaProIleProSerSerArgGly 60  
DB 144 AGCACCCAGCTGCTGCTGCCAAGGCGAAGCGGTGCTCCCAAAACCCAGCAGCCGGGCG 203  
QY 61 GluTyrValAlaAlaLysLeuAspAspLeuValAsnTPAlaArgSerSerLeuTyr 80  
DB 204 GAGTATGTGTGGCCAAAGCTGGATGACCTGTCACACTGGCCCCCGAGTCTCTGTGG 263  
QY 81 PrometThrPheGlyLeuAlaCysGlyAlaValGluMetMetHisMetAlaAlaProArg 100  
DB 264 CCCATGACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323  
QY 101 TyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMet 120  
DB 324 TACGACATGAGCACCGCTTTGGCGTGTCTTCGCCGCCAGCCCGCGCAAGTCCGACGTCTAG 383  
QY 121 IleValAlaGlyThrIleuThrAsnLysMetAlaProAlaLeuArgLysValTyrAspGln 140  
DB 384 ATCTGGCCCGGACACCTCACCAACAGATGAGCCCGCTTCCGAGGTCTACGACGAC 443

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Qy 141 MetProGluProArgTyrValValSerMetGlySerCysAlaAenglyGlyTyrTyr 160
Db 444 ATGCCGGAGCCGCCCTACGTGCTCCATGGGAGCTCGCCCAACGAGAGGCTACTAC 503
Qy 161 HistYserTyrSerValValArgGlyCysAspArgIleValProValAspIleTyrIle 180
Db 504 CACTATTCTCACTCGGTGTAGGGGCTGCACCGCATCTGCGCCGTGGACATCTACATC 563
Qy 181 ProGlyCysProProthAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgIys 200
Db 564 CCAGCTGCTCCCACTCCGCGGAGGCTGCTCTACGGCATCTGCACTGCAAGGAG 623
Qy 201 IleYsaArgGluArgArgLeuGlnIleTyrTyrArgArg 213
Db 624 ATCAAGCGGAGCGGAGGCTGCATCTGTACCGCAG 662

RESULT 3
US-10-104-047-625
; Sequence 625, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 625
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-625

Alignment Scores:
Pred. No.: 3,16e-114 Length: 2818
Score: 965.00 Matches: 186
Percent Similarity: 96.88% Conservative: 0
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 86.31% Indels: 4
DB: 17 Gaps: 1

US-09-525-867-1 (1-213) x US-10-104-047-625 (1-2818)
Qy 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20
Db 24 ATGCGCGGTGCTGACGCTCTGCGCTGCGCGCTTCCGGATCTT3GTCTGCTCCAGC 83
Qy 21 ValGlyProAlaValGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
Db 84 GTGGGCCCCGGCTGTGCAGGACGAGGTGTCCATCAGACGTGGCCACCGAGTGGCCCAAGC 143
Qy 41 SerThrGlnProAlaLeuProLyAlaArgAlaValAlaProLySProSerSerArgGly 60
Db 144 AGCACCCAGCTGCTGCCCTGCCAAGGCCAGACCGGTGCTCCCAACCAAGACGCCGGGC 203
Qy 61 GluTyrValValAlaValSLeuAspAspLeuValAsnTrpAlaArgArgSerSerLeuTrp 80
Db 204 GAGATATGTGTGGCCCAAGCTGATGACTCTGTCACATGGGCCCGCGGAGTTCTCTGTG 263
Qy 81 ProMetThrPheGlyLeuAlaCysCysAlaValAlaGlnMetMetHisMetAlaAlaProArg 100
Db 264 CCCATGACCTTGGCTGTGGCTGTGCGCCGTGGAGATGATGACATGGCAGCACCCCGC 323
Qy 101 TyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSerAspValMet 120
Db 324 TAGACATGAGACCGCTTTGGGTGTCTTCCGGCGCAGCCCGCTCCAGTCCGACGTATG 383
Qy 121 IleValAlaGlyTyrLeuThrAsnLyMetAlaProAlaLeuValGlyValTyrAspGln 140
Db 384 ATCTGTGGCGGACACATCACCAACAGATGGCCCGACGCTTTCGCAAGTCTACGACACAG 443
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Qy 141 MetProGluProArgTyrValValSerMetGlySerCysAlaAenglyGlyTyrTyr 160
Db 444 ATGCCGGAGCCGCCCTACGTGCTCCATGGGAGCTCGCCCAACGAGAGGCTACTAC 503
Qy 161 HistYserTyrSerValValArgGlyCysAspArgIleValProValAspIleTyrIle 180
Db 504 CACTATTCTCACTCGGTGTAGGGGCTGCACCGCATCTGCGCCGTGGACATCTACATC 563
Qy 181 ProGly-----CysProProthAlaGlu 188
Db 564 CCAGTATGGCGCGGAGCCGACCGCACCGCACGAGGAG 599

RESULT 4
US-10-104-047-914
; Sequence 914, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 914
; LENGTH: 3089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-914

Alignment Scores:
Pred. No.: 1.23e-104 Length: 3089
Score: 891.50 Matches: 185
Percent Similarity: 68.01% Conservative: 0
Best Local Similarity: 79.74% Mismatches: 3
Query Match: 17 Indels: 85
DB: 17 Gaps: 2

US-09-525-867-1 (1-213) x US-10-104-047-914 (1-3089)
Qy 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20
Db 53 ATGCGGTGCTGTACGCTCTGCGCTGCGCGCTTCCGGATCTTGGTCTGCTCCAGC 112
Qy 21 ValGlyProAlaValGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
Db 113 GTGGGCCCCGGCTGTGCAGGACGAGGTGTCCATCAGACGTGGCCACCGATGGCCCAAG- 171
Qy 40 ----- 40
Db 172 CAGGTGAAGCTGACCTTCTGGGGAGGTGTACCCCTCGCCCAACCCCATCTTCCT 231
Qy 40 ----- 40
Db 232 TATTTTCTGATCAGTCCCGCAGCCACTGAGTGCATGATGGGCGAGGAGGGGTAC 291
Qy 40 ----- 40
Db 292 ACATCCAGTCTCTGACCTCATGTGGGTCCAGGCTCTGGCAGGCGCGTGGGGCTGCG 351
Qy 40 ----- 40
Db 352 ATCCGCTCTGGGAGGACCTGCTGGCTGACGCTCTGTGCTGTGTCTGTGCTC 411
Qy 41 SerThrGlnProAlaLeuProLyAlaArgAlaValAlaProLySProSerSerArgGly 60
Db 412 AGCACCCAGCTGCTGCCCTGCCAAGGCCAGACCGGTGCTCCCAACCAAGACGCCGGGC 471
Qy 61 GluTyrValValAlaValSLeuAspAspLeuValAsnTrpAlaArgArgSerSerLeuTrp 80
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Db      472 GAGTATGTGTGGCCAGAGCTGATGACCTCTGCACTGGGCCCGGAGTTCTCTGTGG 531
Qy      81  PrometThrPheGlyLeuAlaValGlyCysAlaValGlyMetMetHsMetAlaValProArg 100
Db      532 CCCATGACCTTGGGCTGGCTGTGGCCCGGTGAGATGATGACATGGACGACCCCG 591
Qy      101  TyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSerAspValMet 120
Db      592 TACGACATGAGACCGCTTGGCGTGGTCTTCCGCCCGGAGCCCGGACGTCGACGTCATG 651
Qy      121  TLeuAlaValGlyThrLeuThrAspLeuMetAlaProAlaLeuArgValTyrAspGln 140
Db      652 ATCGTGGCCGGACACTACCAACAGATGAGCCCGGCTTCCGCAAGGCTTACGACCA 711
Qy      141  MetProGluProArgTyrValValSerMetGlySerCysAlaAsnGlyValGlyTyrTyr 160
Db      712 ATGCGGAGCCGCTGACGTCGTCATGCGGAGCTGCGCAACGAGAGGCTTACATAC 771
Qy      161  HisTyrSerTyrSerValValArgGlyCysAspArgTyrValProValAspTyrTyrTyr 180
Db      772 CACTATTCCTAATCGGTGGTGAAGGGCTCGACCGCATCTGTGCCGTGACATCTACATC 831
Qy      181  ProGly-----CysProProThrAlaGlu 188
Db      832 CCAGGTAGGGCCGGACCGCACCGCCACGAGGGAG 867

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RESULT 5
US-10-104-047-262
; Sequence 262, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 262
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-262

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Alignment Scores:
Pred. No.:      6,05e-101      Length:      3050
Score:          863.00      Matches:      166
Percent Similarity: 95.40%      Conservative: 0
Best Local Similarity: 95.40%      Mismatches: 4
Query Match:      77.19%      Indels:      4
DB:              17          Gaps:      1

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US-09-525-867-1 (1-213) x US-10-104-047-262 (1-3050)

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Qy      19  SerSerValGlyProAlaValGlnAlaArgGlyValHisGlnSerValAlaThrAspGly 38
Db      307 TCCAGCGTGGCCCTGGCTGTGACGACGAGGTGTCATCAGAGCGTGGCCACCATGAC 366
Qy      39  ProSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLysProSerSer 58
Db      367 CCAAGCAGACCCAGCCTGCTGCGCAAGAGCCAGAGCCCTGCTCCCAACCCAGAGCG 426
Qy      59  ArgGlyGluTyrValValAlaValLeuAspLeuValAsnTyrPalaArgArgSerSer 78
Db      427 CGGGGCGAGTATGTGTGGCCAGAGCTGATGACCTCGTCACTGGGCGCCGCGAGTTCT 486
Qy      79  LeuTyrProMetThrPheGlyLeuAlaCysCysAlaValGlyMetMetHsMetAlaAla 98
Db      487 CTGTGCGCATATGACCTTGGCTGCTGCGCGCGCGGAGATGATGACATGGAGGAGCA 546
Qy      99  ProArgTyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSerAsp 118

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Db      547 CCGCGTACAGACATGAGCGGCTTGGCGGTGCTTCCGCGCAGCCCGCGCACCCGAC 606
Qy      119  ValMetTyrValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgValTyr 138
Db      607 GTCATATGATGATGGCGGACACTCACCAACAGATGCGCCCGGCTTCCGAGGTCTAC 666
Qy      139  AspGlnMetProGlyProArgTyrValValSerMetGlySerCysAlaAsnGlyGlyGly 158
Db      667 GACCAAGATCCGAGACCCCGCTACGATGCTTCATGAGGAGCTGCGCAACGAGGAGCG 726
Qy      159  TyrTyrHisTyrSerTyrSerValValArgGlyCysAspArgTyrValProValAspTyr 178
Db      727 TACTTACCATATTCCTACTCGGTGTGAGGGGCTGGGACCGCATCTGTGCGGTGACATC 786
Qy      179  TyrTyrProGly-----CysProProThrAlaGlu 188
Db      787 TACATCCAGGTAGGCGCGGAGCCGACCGCCACGAGGGAG 828

```

```

RESULT 6
US-10-767-701-19893
; Sequence 19893, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 2004-01-29
; SEQ ID NO 19893
; LENGTH: 797
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(797)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB5049-010-R1-XP1-F9
US-10-767-701-19893

```

```

Alignment Scores:
Pred. No.:      3,65e-86      Length:      797
Score:          743.00      Matches:      144
Percent Similarity: 72.53%      Conservative: 25
Best Local Similarity: 61.80%      Mismatches: 40
Query Match:      66.46%      Indels:      24
DB:              18          Gaps:      3

```

US-09-525-867-1 (1-213) x US-10-767-701-19893 (1-797)

```

Qy      1  MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgTyrLeuGlyLeuArgSerSer 20
Db      34  ATGTGTCTATTAATCAACCAAGGTCTCCGAAC-----GGCTCTCAAGAGCTCG 81
Qy      21  -----ValGlyProAlaValGlnAla 27
Db      82  TCTTCTCTCAAGACCACTTGGCATTCGACGACCACTCTCCACATCGGCATCGCT 141
Qy      28  ArgGlyValHisGlnSerValAlaThrAspGlyProSerSerThrGlnProAlaLeuPro 47
Db      142  CGTAAACCAATTCCTTCCATTAATGATATGATCGGACCATCTCCATCAATCAATCAATCA 201
Qy      48  LysAlaArgAla-----ValAlaProLysProSerSerArgGly 60
Db      202  ACTAGAACAGCTCAAGAGGTTCAACCAACTTCTTGAACCTCCACGAAAGCGGCGCT 261
Qy      61  GluTyrValValAlaValLeuAspLeuValAsnTyrPalaArgArgSerSerLeuTyr 80

```

Db 262 GAATATGCTTGTGCACTCTGATTAATAATGGCTCAATTTGGGCTAGACAAAGTTTCGATGTGG 321  
Qy 81 PrometThrPheGlyLeuAlaCysCysAlaValaGluMetMetHisMetAlaAlaProArg 100  
Db 322 CCGATGACTTTCGGTTTGCTGTGGTCCCGGAGAGATGATGACATGCTGCTGCTAGA 381  
Qy 101 TyrAspMetAspArgPheGlyValaValaPheArgAlaSerProArgGlnSerAspValMet 120  
Db 382 TATGACCAAGATTCAGTTGGGTGTGTGTTCGAGCCAGTCCCTCGACAAAGATATCATG 441  
Qy 121 TleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValaTyrAspGln 140  
Db 442 ATATAGCCGGGTACATTGACCAACAAAGATGGCGCAGCTCTTGGAAAGGTCTACGATCA 501  
Qy 141 MetProGluProArgTyrValaValaSerMetGlySerCysAlaAsnGlyGlyGlyTyrTyr 160  
Db 502 ATGCCAGAACCAAGATGGGTCAATTCTATGGGTCTTGTGCCAAGAGAGAGTTACTAC 561  
Qy 161 HisTyrSerTyrSerValaValaArgGlyCysAspArgIleValaProValaAspIleTyrIle 180  
Db 562 CACTACTGTACTGTGTGTGAGAGTTGTGACCGTATAGTTCCCGTTGACATTTAGCTC 621  
Qy 181 ProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgLys 200  
Db 622 CCAGAGATGTCCACCCACCTGCGAGGCTGTGTGACGGTATGCTTGCCCTTCAGCGAAG 681  
Qy 201 IleLysArgGlyArgArgLeuGlnIleTyrTyrArgArg 213  
Db 682 ATGCCAGAACCAAGACGCGCGCTCATGTGTACAGAAAA 720

## RESULT 7

US-10-767-701-14502  
; Sequence 14502, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 14502  
; LENGTH: 1092  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-CLUS4585\_1  
US-10-767-701-14502

## Alignment Scores:

Pred. No.:	1,18e-85	Length:	1092
Score:	740.50	Matches:	144
Percent Similarity:	75.12%	Conservative:	19
Best Local Similarity:	66.36%	Mismatches:	46
Query Match:	66.23%	Indels:	8
DB:	18	Gaps:	2

US-09-525-867-1 (1-213) x US-10-767-701-14502 (1-1092)

Qy 4 LeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValaGlyPro 23  
Db 73 CTTCACGCCCTCTCTCCACAGAGTGAGAAACCTTAGCAGCCAGACATGCGCTGCTCC 132  
Qy 24 AlaValGlnAlaArgGly-Val-----HisGlnSerValAlaThrAs 37  
Db 133 GCGACGCGCGCGCGCTCTCTCTCACTCCGCGGCGCTACTCCGCGCGCTGCTGC 192  
Qy 37 pGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLysProSe 57  
Db 193 GGGGGCCTCTCTGACGTCCAGCG---CATATACGGGGCGCGCCCGCGCGCATGTC 249

Qy 57 rSerArgGlyGlyTyrValaValaLysLeuAspAspLeuValaSerTrpAlaArgSe 77  
Db 250 GAACAGCGCCAGATTCTGTGTGCTCCCAAGCTGACGACTGATGAACTGGCGCTAGAGG 309  
Qy 77 rSerLeuTrpProMetThrPheGlyLeuAlaCysCysAlaValaGluMetMetHisMetAl 97  
Db 310 CTCGATCTGGCCCATGACCTTCGGGGCTGCTGCTGCGCGGTGAGATGATGACAGCCGG 369  
Qy 97 aAlaProArgTyrTrpSerMetAspArgPheGlyValaValaPheArgAlaSerProArgGln 117  
Db 370 CGCTCCCGCTACGACTTCGACCGGTTGCGGTATCTTCCTGCTGCGCGCACTC 429  
Qy 117 rAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVa 137  
Db 430 CGATTGCAATGATCTCCCGGACAGCTCACCAACAAATGGCTCAGCCCTCCGCAAGT 489  
Qy 137 TTrpAspGlnMetProGluProArgTyrValaValaSerMetGlySerCysAlaAsnGly 157  
Db 490 TTATGACCAAAATGCTGAGCCTAGAGGTATTTCAATGGGCAAGCTGTGCCAAGCTGG 549  
Qy 157 YGlyTyrTyrHisTyrSerTyrSerValaValaArgGlyCysAspArgIleValaProVala 177  
Db 550 TGGATCTACCATTACTCTACTCTGTGTGACGTGAGATGACCGTATAGTCCCTGAGA 609  
Qy 177 PileTyrIleProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLe 197  
Db 610 CATCTACGTCCTCTGCGGTGCGCCACCAACTGCTGAGGCACTAGTACGCTTCTTCACT 669  
Qy 197 uGlnArgLysIleLysArgGlyArgArgLeuGlnIleTyrTyrArgArg 213  
Db 670 CCAAAAGAAAGATCAACAGCGCTAGAGATTCTTCACTGCTGAGCAAG 718

## RESULT 8

US-10-425-114-16284  
; Sequence 16284, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 16284  
; LENGTH: 886  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3062-027-H6\_FLI  
US-10-425-114-16284

## Alignment Scores:

Pred. No.:	2,18e-85	Length:	886
Score:	737.50	Matches:	143
Percent Similarity:	75.70%	Conservative:	19
Best Local Similarity:	66.82%	Mismatches:	44
Query Match:	65.97%	Indels:	8
DB:	17	Gaps:	2

US-09-525-867-1 (1-213) x US-10-425-114-16284 (1-886)

Qy 7 ProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValaGlyProAlaValaGln 26  
Db 9 CCTGCTCACGAGGTGAGAAACCTTAGCAGCACCAACATGCGCTTGTCTCCGCGCACCGC 68  
Qy 27 AlaArgGly-Val-----HisGlnSerValAlaThrAspGlyProSe 40

```

Db      69 GCGGCTGGCCCTCTTCCACCCCGGCGCTACTCCGCTGCGCGCTGCGCGCGCTC 128
      40 rSerThrGlnProAlaLeuProlysalAlaValAlaProlyProSerSerArg1 60
      129 CCCGACCTGCCACGG--CCATACGGGGGCGCGCCCCCACCGGCGATGTCGAACACGGC 185
      60 yGluTyrValAlaAlaIleuAspAspLeuValaenTPAlaArgArgSerSerLeuTr 80
      186 CGAGTTCGTGCTCTTAAGGTGACGACCTGATGAACGTGGCGCTGAAGCGCTCATCTG 245
      80 pPrometThrPheGlyLeuAlaCysCysAlaValaGluMetMetHisMetAlaAlaProAr 100
      246 GCCCATGACCTTGGGCTGCGCTGCGCGCGGTGAGATGATGACACCGCGCGCGCTCCG 305
      100 gTyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgInSerAspValMe 120
      306 CTACGACTTCGACCGGCTGCGGCTCATCTCCGCTCGCGCGCGCAAGTCCGATTCAT 365
      120 tIleValAlaGlyThrLeuThrAsnIleMetAlaProAlaLeuArgIleValaTyrAspG1 140
      366 GATCGCGCGCGGACGCTCACCAACAGATGCTCCGCGCTCCGCAAGGTTTATGACCA 425
      140 nMetProGlnProArgTyrValAlaSerMetGlySerCysAlaAsnGlyGlyGlyTyrTy 160
      426 AATGCTGAGCCTAGGTGGTTATTCAATGGGCACTGTCACACGCGTGTGATGATCTA 485
      160 rHisTyrSerTyrSerValAlaArgGlyCysAspArgIleValaProValAspIleTyr11 180
      486 CCATTACTCTTACTCTGTGTGACGTGATGACCGATATGTCCTCTGTGACATCTACGT 545
      180 eProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgly 200
      546 CCCGGGTGGCCACCACTGCTGAGGACATGCTGTCACGGGCTTCTTCACTCCAAAGAA 605
      200 sIleLysArgGlnArgIleuGlnIleTyrTyrArgArg 213
      606 GATCAACAGCGCTAAGGATTTCTTCACTGTGACCAAG 645

```

RESULT 9

```

US-10-425-114-6711
; Sequence 6711, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 6711
; LENGTH: 949
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700576010_FLI
US-10-425-114-6711

```

Alignment Scores:

```

Pred. No.: 2,39e-85 Length: 949
Score: 737.50 Matches: 143
Percent Similarity: 75.70% Conservative: 19
Best Local Similarity: 65.82% Mismatches: 44
Query Match: 65.97% Indels: 8
DB: 17 Gaps: 2

```

\* US-09-525-867-1 (1-213) x US-10-425-114-6711 (1-949)

```

      7 ProGlyLeuArgGlyPheArgIleuGlyLeuArgSerSerValaGlyProAlaValaGln 26
      29 CCTCGTCACGAGGTGAGGAAACCTTACGACCAACATGAGCTGTGCTCCCGGCGCACCGC 88
      27 AlaArgGly-Vala-----HisGlnSerValaAlaThrAspGlyProse 40
      89 GCGGCTGGCCCTCTTCCACCCCGGCGGCTACTCCGCTGCGCGCTGCTCCGCGCGCTC 148
      40 rSerThrGlnProAlaLeuProlysalAlaValAlaProlyProSerSerArg1 60
      149 CCCGACCTGCCACGG--CCATACGGGGGCGCGCCCCCACCGGCGATGTCGAACACGGC 205
      60 yGluTyrValAlaAlaIleuAspAspLeuValaenTPAlaArgArgSerSerLeuTr 80
      206 CGAGTTCGTGCTCTTAAGGTGACGACCTGATGAACGTGGCGCTGAAGCGCTCATCTG 265
      80 pPrometThrPheGlyLeuAlaCysCysAlaValaGluMetMetHisMetAlaAlaProAr 100
      266 GCCCATGACCTTGGGCTGCGCTGCGCGGTGAGATGATGACACCGCGCGCGCTCCG 325
      100 gTyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgInSerAspValMe 120
      326 CTACGACTTCGACCGGCTGCGGCTCATCTCCGCTCGCGCGCGCAAGTTCATTCAT 385
      120 tIleValAlaGlyThrLeuThrAsnIleMetAlaProAlaLeuArgIleValaTyrAspG1 140
      386 GATCGTCGCGCGGACGCTCACCAACAGATGCTCCGCGCTCCGCAAGGTTTATGACCA 445
      140 nMetProGlnProArgTyrValAlaSerMetGlySerCysAlaAsnGlyGlyGlyTyrTy 160
      446 AATGCTGAGCCTAGGTGGTTATTCAATGGGCACTGTCACACGCGTGTGATGATCTA 505
      160 rHisTyrSerTyrSerValAlaArgGlyCysAspArgIleValaProValAspIleTyr11 180
      506 CCATTACTCTTACTCTGTGTGACGTGATGACCGATATGTCCTCTGTGACATCTACGT 565
      180 eProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgly 200
      566 CCTGGGTGGCCACCACTGCTGAGGACATGCTGTCACGGGCTTCTTCACTCCAAAGAA 625
      200 sIleLysArgGlnArgIleuGlnIleTyrTyrArgArg 213
      626 GATCAACAGCGCTAAGGATTTCTTCACTGTGACCAAG 665

```

RESULT 10

```

US-10-425-115-3877
; Sequence 3877, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 3877
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MWT4577_103539C.1
US-10-425-115-3877

```

Alignment Scores:

```

Pred. No.: 4.03e-85 Length: 1394
Score: 737.50 Matches: 143
Percent Similarity: 75.70% Conservative: 19
Best Local Similarity: 66.82% Mismatches: 44

```

Query Match: 65.97% Indels: 8  
DB: 18 Gaps: 2  
US-09-525-867-1 (1-213) x US-10-425-115-3877 (1-1394)

```
QY 7 ProGlyLeuArgGlyPheArgIleuGlyLeuArgSerSerValGlyProAlaValGln 26
DB CCTGTCACACGAGGTGAGGAAACCTTAGCCGACCCGACCTAGCGGTGGTCCCGCCACCGC 299
QY 27 AlaArgGlyVal-----HisGlnSerValAlaThrAspGlyProse 40
DB 300 GCGGCTGGCCCTCTCCACCAGCGGGCGGCTACTCCGCTCCGCTGCTGGGGGCGCTC 359
QY 40 rSerThrGlnProAlaLeuProValAlaArgAlaValAlaProLysProSerSerArgG1 60
DB 360 CCCGACGCCCCACGCG---CCATACGGGGGGGGGGCCCCCGGCGGAGTGTGAAGACGCG 416
QY 60 yGluTrValValAlaValLeuAspAspLeuValAsnTrpAlaArgAlaSerSerLeuTr 80
DB 417 CGAGTTGCTGGTCTTAGAGTGAAGACCTGATGAACTGGGCGGCTAAGGCTCGATCTG 476
QY 80 pPromethrPheGlyLeuAlaCy8Cy8AlaValGluMetMetHisMetAlaAlaProAr 100
DB 477 GCCCATGACCTTCGCGGCTCGGCTGCTGCGCGAGTGAATGACACGCGGCGGCTCCG 536
QY 100 gTYrAspMetAspArpPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMe 120
DB 537 CTACGACTTCGACCGGCTTCGCGCTCATCTTCGCTCCGCGCGCGCGCTCGATTCGAT 596
QY 120 tLeValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValTYrAspG1 140
DB 597 GATCGTCGCGCGGACGCTCACCAACAGATGCTCCGCGCTCCGCAAGTTTATGACCA 656
QY 140 mMetProGlnProArgTrpValAlaSerMetGlySerCy8AlaAsnGlyGlyTYrTY 160
DB 657 AATCCCTGAGGCTGAGTGGTATTTCATATGAGGACGCTGCCAACGCTGTGATGACTA 716
QY 160 rHisTYrSerTYrSerValAlaArgGlyCy8AspAspArgLLeValProValAspIleTYr11 180
DB 717 CCATTACTCTTCACTCTGTGTGATGATGATGACCGTATGACTCCTCTGCGACACTTACT 776
QY 180 eProGlyCy8ProProThrAlaGluAlaLeuLeuTYrGlyTleLeuGlnLeuGlnArgL 200
DB 777 CCTGGGAGGCCACCAACTGCTGAGGACACTGCTGACGCGCTTCTTACGTCCAAAAGAA 836
QY 200 gIleLeuArgGluArgArgLeuGlnIleTrpTYrArgArg 213
DB 837 GATCAACAGGCGTAAGATTCTTCACTGATGGACCAAG 876
```

RESULT 11  
US-10-425-115-3875

Sequence 3875, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 3875  
LENGTH: 1840  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_103537C.1  
US-10-425-115-3875

Alignment Scores:

Pred. No.: 1,07e-84 Length: 1840  
Score: 735.50 Matches: 144  
Percent Similarity: 74.65% Conservative: 18  
Best Local Similarity: 66.36% Mismatches: 47  
Query Match: 65.79% Indels: 8  
DB: 18 Gaps: 2

```
US-09-525-867-1 (1-213) x US-10-425-115-3875 (1-1840)
QY 4 LeuSerAlaProGlyLeuArgGlyPheArgIleuGlyLeuArgSerSerValGlyPro 23
DB 819 CTTCGCTCTCTCTCCACGAGGTGAGGAAACCTTAGCCGACCTAGCGGTGGTCTCC 878
QY 24 AlaValGlnAlaArgGly-----Val-HisGlnSerValAlaThrAs 37
DB 879 GCGGACCGCACGAGTGGGCTTCTCTCTACCCCGGCTCGTACTCCCGCGCGCGCTGC 938
QY 37 pGlyProSerSerThrGlnProAlaLeuProValAlaArgAlaValAlaProLysProse 57
DB 939 GGGGCGCTCCCGACCTCCCGACGCG---CCATACGGGGGGCGCGCCCCCGCGGATGTC 995
QY 57 rSerArgGlyGluTrpValValAlaValLeuAspAspLeuValAsnTrpAlaArgArgse 77
DB 996 GAAGACGCGCGAGTTCGTGCTCCAGAGTTGATGACTGTATGAACTGGGCGCGCTAAGCG 1055
QY 77 rSerLeuTrpPromethrPheGlyLeuAlaCy8Cy8AlaValGluMetMetHisMetAl 97
DB 1056 CTCGATTGGGCCCATGACCTTCGCGGCTGCTGCTGCGCGCTCGAGATGATGACGCGCG 1115
QY 97 aAlaProArgTrpAspMetAspArpPheGlyValAlaPheArgAlaSerProArgGlnse 117
DB 1116 GCGCTCCCGCTACGACTTCGACCGGTTGCGGCTGATCTTCGCTCCGCTCCGCGCGCACTC 1175
QY 117 rAspValMetLeValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVa 137
DB 1176 CGATTGATGATGCTCTCCCGGACGCTCACCAACAAATGCTCCAGCTCCGCAAGCT 1235
QY 137 TYrAspGlnMetProGlnProArgTrpValAlaSerMetGlySerCy8AlaAsnGlyG1 157
DB 1236 TTATGACCAAAATGCTGACCTTACGCTTATGATGGGACAGCTGTGCCAACGCTGCG 1295
QY 1296 TGATATGACCATTAATCTCTCTCTGTGTGATGATGATGATGATGATGATGATGATG 1355
QY 157 yGlyTYrTYrHisTYrSerTYrSerValAlaArgGlyCy8AspAspArgLLeValProValAs 177
DB 1296 TGATATGACCATTAATCTCTCTCTGTGTGATGATGATGATGATGATGATGATGATG 1355
QY 177 pIleTYrIleProGlyCy8ProProThrAlaGluAlaLeuLeuTYrGlyTleLeuGlnLe 197
DB 1356 CATCTACGTCTCTGAGTGGGCCACCAACTGCTGAGGACACTGCTGTACGCTGTTCACGCT 1415
QY 197 uGlnArgLysIleLeuArgGluArgArgLeuGlnIleTrpTYrArgArg 213
DB 1416 CCMAAGAGATCAACAGGCGTAAAGATTCTTCACTGATGGAGCAAG 1464
```

RESULT 12  
US-10-320-797-2049

Sequence 2049, Application US/10320797  
Publication No. US20040014955A1  
GENERAL INFORMATION:  
APPLICANT: Eroshkin, Alexey M.  
APPLICANT: Zamudio, Carlos  
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND  
FILE REFERENCE: 10182-021-999  
CURRENT APPLICATION NUMBER: US/10/320,797  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: 60/341,261  
NUMBER OF SEQ ID NOS: 3361  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2049  
LENGTH: 753  
TYPE: DNA  
ORGANISM: Cryptococcus neoformans

US-10-320-797-2049

## Alignment Scores:

Pred. No.:	1.05e-84	Length:	753
Score:	731.50	Matches:	140
Percent Similarity:	72.69%	Conservative:	17
Best Local Similarity:	64.81%	Mismatches:	18
Query Match:	65.43%	Indels:	41
DB:	17	Gaps:	2

US-09-525-867-1 (1-213) x US-10-320-797-2049 (1-753)

```

QY 39 ProSerSerThrGlnProAlaLeuProlysaIaArg-----AlaValAla 53
DB 103 CCGGCGCGGTTCAGACCCGCACTGCACCTCGCTCCGCTCCGTCACAGACCGCGCTGCC 162
QY 54 ProLys----- 55
DB 163 CCGAGGCCCAACACACACCACTCGGCATCACTCGTACACCACTCGCCCTCCACCACT 222
QY 56 -----ProSer 57
DB 223 CTGCCAGACACCACTCGCCCAAGAAAGACCACTTGAGTCTCGAGACACTAGA 282
QY 58 SerArgGlyIuTyValAlaValAlaLysLeuAspAspLeuValAsnTrpAlaArgSer 77
DB 283 AACGCGCCGAGTATGCTCTTCAACGCTCGACACAAATGTCACCTGCGGCGCAAGG 342
QY 78 SerLeuTrpProMetThrPheGlyLeuAlaCysCysAlaValGlnMetMetHisMetAla 97
DB 343 TCCATGTGCGCCCAATGACTTGTGCTCGCTCGCTGCGCGCGTGAATGATGCATGCT 402
QY 98 AlaProArgTyraAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSer 117
DB 403 GCGCGCCGATATGATCAAGATGACCTCGGTCTGCTTCCGAGCGTCCCGGACAGAGT 462
QY 118 AspValMetLeuValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVal 137
DB 463 GATGTTATGATGTGTACAGACTCTTAAACAAAGATGCTGCTGCGTTAGAGAAAGTG 522
QY 138 TyrAspGlnMetProGlnProArgTyraValAlaSerMetGlySerCysAlaAsnGlyGly 157
DB 523 TACGACCAATGCGCGAACCAGGAGGCTCATTTCTAAGGTTGTCATGGCCCAATGGCGGT 582
QY 158 GlyTyrrTyrrHisTyrrSerTyrrSerValAlaArgGlyCysAspArgLeuValProValAsp 177
DB 583 GGCTACTACACTACTCTGCTCGGTGCGAGGCTGTGACCGAATCGTCCCTGTGAC 642
QY 178 IleTyrrIleProGlyCysProProThrAlaGlnAlaLeuLeuTyrrGlyIleLeuGlnLeu 197
DB 643 ATCTATGTCCCGGATGCTCTCCACCGCGCGGCGCTTCTTAAGGAATGCTCAATTA 702
QY 198 GlnArgLysIleLysArgGlnArgGlnLeuGlnIleTyrrTyraArg 213
DB 703 ATGCGAAGATGAGGCGGTAAACAGACAGTGTGCGATGTAACGAGAG 750

```

RESULT 13

US-10-424-599-6216/c

Sequence 6216, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424, 599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 6216

LENGTH: 1356

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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105622C.1
US-10-424-599-6216

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## Alignment Scores:

Pred. No.:	4.92e-84	Length:	1356
Score:	729.00	Matches:	137
Percent Similarity:	76.53%	Conservative:	26
Best Local Similarity:	64.32%	Mismatches:	50
Query Match:	65.21%	Indels:	0
DB:	17	Gaps:	0

US-09-525-867-1 (1-213) x US-10-424-599-6216 (1-1356)

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QY 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSer 20
DB 1236 ATGGCTCTTCTGATGTCAGGCTCTTCAACGCTTCCCTCCACCTGTTCCCTCAAGAGTT 1177
QY 21 ValGlyProAlaValAlaGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
DB 1176 GTTTCCTCCACCAACAGCTCCCATCTCTTAACGATCAACATCCACACCGCCGCC 1117
QY 41 SerThrGlnProAlaLeuProlysaIaArgAlaValAlaProLysProSerSerArgGly 60
DB 1116 CCATATGCCCGCCACCGGCTCCGCTCCCTCCCGCGCGGTGCGAGGCGGCG 1057
QY 61 GlnTyrrValAlaValAlaLysLeuAspAspLeuValAsnTrpAlaArgSerSerLeuTrp 80
DB 1056 GAGTTCGTATCTCGAAGGTGACATCTGATGAACTGGCCGCGCGGCTCATCTGG 997
QY 81 PromMetThrPheGlyLeuAlaCysCysAlaValGlnMetMetHisMetAlaAlaProArg 100
DB 996 CCATATGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
QY 101 TyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMet 120
DB 936 TACGATCTGACCGGCTTGGCATCATTTTACAGGCCGACCCCTGCGCATGTCATG 877
QY 121 IleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValTyrAspGln 140
DB 876 ATGTCGTCGACACTCTCACCAACAAAGATGCTCCCTCTGCAAGGTTATGACCA 817
QY 141 MetProGlnProArgTyrrValAlaSerMetGlySerCysAlaAsnGlyGlyTyrr 160
DB 816 ATGCTGAGCTTAATGAGTGTCTCAATGAGAAATGTCATATGAGAGAGATCTAC 757
QY 161 HisTyrrSerTyrrSerValAlaArgGlyCysAspArgIleValProValAspIleTyrrIle 180
DB 756 CATTACTCTTAATCTCCGATGTCGGGAGTGTGACAGAGATTGTTCTGTGACATATATAT 697
QY 181 ProGlyCysProProThrAlaGlnAlaLeuLeuTyrrGlyIleLeuGlnLeuGlnArgLys 200
DB 696 CCAAGCTGTCTTCAACTGCTGAGGCTTGTGCTGTATGATGACTCTCCACGTCGAGAAAAAG 637
QY 201 IleLysArgGlnArgGlnLeuGlnIleTyrrTyraArg 213
DB 636 ATCAATAGGCGCAAGACTTCTCATGTGTGAGCAAAAG 598

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RESULT 14

US-10-425-114-36399

Sequence 36399, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Lin, Jindong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven B

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With



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; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36399
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZKROTBSINT093D10_FLI
US-10-425-114-36399

Alignment Scores:
Pred. No.: 5.63e-84      Length: 863
Score: 726.50          Matches: 133
Percent Similarity: 84.09%      Conservative: 15
Best Local Similarity: 75.57%    Mismatches: 27
Query Match: 64.98%           Indels: 1
DB: 17                  Gaps: 1

US-09-525-867-1 (1-213) x US-10-425-114-36399 (1-863)
Qy      38 GlyProSerSerThrGlnProAlaLeuProlysaAlaArgAlaValAla) aProLyseProSer 57
Db      4 GGCCTCTCCCGGAGCTCCCGCAGCG--CCATACGGGGGGGCGCCCGCCACCGCGCATGTGC 60
Qy      58 SerArgGlyGlyValValAlaValLeuAspAspLeuValaAntProAlaArgSer 77
Db      61 AAGACGGCGCGAGTCTGAGTCTCTAAGGTGAGACGACTGATGAAGTGGCGCGTAAGGGC 120
Qy      78 SerLeuTrpPrometThrPheGlyLeuAlaCyseCyseAlaValaGluMetMetH) sMeAla 97
Db      121 TCGATCTGGCCCATGACCTTGGGGCTGCGCGCGGTGCGGAGATGATGACAGCGCGC 180
Qy      98 AlaProArgTrpAspMetAspArgPheGlyValValaPheArgAlaAspProArgGlnSer 117
Db      181 GCGCTCCGCTACGACTTCGACCGGTTCGCGCTCTCTCCGCTCCGCGCGCAGTCC 240
Qy      118 AspValMetLeuValaAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgLyseVal 137
Db      241 GATTGCATGATCGTCGCGCGCAGCTCACCAACAGATGGCTCCGCGCTCCGCGAGGTT 300
Qy      138 TyrAspGlnMetProGluProArgTrpValValaSerMetGlySerCyseCyseAlaAsnGly 157
Db      301 TATATACCAATGCTGAGGCTGAGGCTGATTTCAATGGGCAAGCTGTGCCAAGCGTGTGT 360
Qy      158 GlyTrpTrpHisTrpSerTrpSerValValaArgGlyCyseAspArgGlyLevalProValaAsp 177
Db      361 GGATATCTACATTACTCTCTACTGTGTGTATGATGTGACCGTATATGATCCGTGTGAC 420
Qy      178 IleTrpTrpLeuProGlyCyseProProThrAlaGluAlaLeuLeuTrpGlyIleLeuGlnLeu 197
Db      421 ATCTACGCTCCTGAGTGCCACCAACGCTGACGACGCTGTACGCGGTCTTCAGCTC 480
Qy      198 GlnArgLyseIleLyseArgGluArgGlnGlnIleTrpTrpArgArg 213
Db      481 CAAGAAGAAATCAACAGCGCTAAGGATTTCTTCACTGCTGTGACCAAG 528

RESULT 15
US-10-424-599-6217/c
; Sequence 6217, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; SEQ ID NO 6217
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1532)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105623C.1
US-10-424-599-6217

Alignment Scores:
Pred. No.: 1.92e-83      Length: 1532
Score: 725.00          Matches: 136
Percent Similarity: 76.53%      Conservative: 27
Best Local Similarity: 63.85%    Mismatches: 50
Query Match: 64.85%           Indels: 0
DB: 17                  Gaps: 0

US-09-525-867-1 (1-213) x US-10-424-599-6217 (1-1532)
Qy      1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgGlyLeuGlyLeuArgSerSer 20
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Qy      21 ValGlyProAlaValaGlnAlaArgGlyValaHisGlnSerValaIleThrAspGlyProSer 40
Db      946 GTTTCATCTCCACACACAGCTCCATCTCTGAACCATCTCCATCCACACAGCCATCA 887
Qy      41 SerThrGlnProAlaLeuProlysaAlaArgAlaValaAlaProLyseProSerSerArgGly 60
Db      886 CCATATGCCCGCCACACCGCGCTCCGCGCTTCTCCCGCGCGGCGTTTCGAAGCGCGC 827
Qy      61 GluTrpValValaAlaValLeuAspAspLeuValaAntProAlaArgGlnSerSerLeuTrp 80
Db      826 GAGTTCGTGATCTCGAAGGTGAGATCTGTGAACATCGGCGCGCGCGCTCATCTGG 767
Qy      81 PrometThrPheGlyLeuAlaCyseCyseAlaValaGluMetMetH) sMeAlaAlaProArg 100
Db      766 CCGATGACCTTGGCGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCG 707
Qy      101 TyrAspMetAspArgPheGlyValaValaPheArgAlaSerProArgGlnSerAspValaMet 120
Db      706 TAGATCTCGACCGCTTCCGATCATTTTACAGCCCGCGCGCGCGCGCGCGCGCGCG 647
Qy      121 IleValaAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgLyseValaIleTrpAspGln 140
Db      646 ATCGTCCCGGCACTCTCACCAACAGATGGCTCCGCTTCCGCAAGTTTATGACCA 587
Qy      141 MetProGluProArgTrpValValaSerMetGlySerCyseCyseAlaAsnGlyGlyTrpTrp 160
Db      586 ATGCTAGACCTTATAGTGGTGTCTCAATGGAAGTGTGTATATGAGAGGATAC 527
Qy      161 HisTrpSerTrpSerValaValaArgGlyCyseAspArgGlyLevalProValaAspIleTrpTrp 180
Db      526 CATTACTCTTAATCCGATAGTTCCGGGATGTGACAGGATTTGCTCTGTGATATATGTT 467
Qy      181 ProGlyCyseProProThrAlaGluAlaLeuLeuTrpGlyIleLeuGlnLeuGlnArgLyse 200
Db      466 CCAAGCTGTCTCTCCAACTGCTGAGAGCTTGTGTATGAGACTTCCAGCTGCGCAAGAAAG 407
Qy      201 IleLyseArgGluArgGlnGlnIleTrpTrpArgArg 213
Db      406 ATCAATAGCGCAAGACTTCTTCCACTGCTGTGACAAAG 368

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Job time : 582 secs
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GenCore version 5.1.6  
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Run on: March 22, 2005, 04:10:57 ; Search time 182 Seconds  
(without alignments)  
1914.983 Million cell updates/sec

Title: US-09-525-867-1

Perfect score: 1118

Sequence: 1 MAVISAPGLGFRILGRSS.....ILOQRKIKRRRLQIYYRR 213

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	772	4	US-09-620-312D-670
2	756.5	67.7	2378	4	US-09-270-767-14895
3	542	48.5	615	4	US-09-248-786A-2825
4	449	40.2	4403765	3	US-09-103-840A-2
5	449	40.2	4411529	3	US-09-103-840A-1
6	440	39.4	966	4	US-09-253-991A-14622
7	436	39.0	690	4	US-09-489-039A-5374
8	436	39.0	696	4	US-09-253-991A-15142
9	433	38.7	735	4	US-09-543-681A-43
10	431.5	38.6	58909	4	US-09-556-002-30
11	428	38.3	640681	4	US-09-790-988-1
12	427.5	38.2	708	4	US-09-540-236-467

13	418	37.4	684	4	US-09-328-352-581	Sequence 581, App
C 14	411	36.8	789	3	US-09-020-956-32	Sequence 32, Appl
C 15	411	36.8	789	3	US-09-030-607-32	Sequence 33, Appl
C 16	411	36.8	789	3	US-09-439-313-32	Sequence 32, Appl
C 17	411	36.8	789	3	US-09-352-616A-32	Sequence 32, Appl
C 18	411	36.8	789	3	US-09-232-149A-32	Sequence 32, Appl
C 19	411	36.8	789	4	US-09-159-812-32	Sequence 32, Appl
C 20	411	36.8	789	4	US-09-636-215-32	Sequence 32, Appl
C 21	411	36.8	789	4	US-09-685-166A-32	Sequence 32, Appl
C 22	411	36.8	789	4	US-09-115-453-32	Sequence 32, Appl
C 23	411	36.8	789	4	US-09-688-489-32	Sequence 32, Appl
C 24	411	36.8	789	4	US-09-679-426-32	Sequence 32, Appl
C 25	411	36.8	789	4	US-09-759-143-32	Sequence 32, Appl
C 26	411	36.8	789	4	US-09-651-236-32	Sequence 32, Appl
C 27	381	34.1	275	4	US-09-313-294A-6583	Sequence 6583, Ap
C 28	373	33.4	513	4	US-09-902-540-4615	Sequence 4615, Ap
C 29	373	33.4	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 30	276	24.7	788	4	US-09-489-039A-2763	Sequence 2763, Ap
C 31	265.5	23.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 32	265.5	23.7	1664976	4	US-09-692-570-1	Sequence 2334, Ap
C 33	265	23.7	810	4	US-09-543-681A-2334	Sequence 2, Appl
C 34	105.5	9.4	4403765	3	US-09-103-840A-2	Sequence 1, Appl
C 35	105.5	9.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 36	104.5	9.3	6663	4	US-09-335-011-15	Sequence 15, Appl
C 37	104.5	9.3	7223	4	US-09-335-011-8	Sequence 8, Appl
C 38	104	9.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 39	104	9.3	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 40	101	9.0	3524	3	US-08-801-344-7	Sequence 7, Appl
C 41	101	9.0	3524	3	US-09-498-399-7	Sequence 7, Appl
C 42	98.5	8.8	16448	4	US-09-902-540-9686	Sequence 9686, Ap
C 43	98.5	8.8	16450	4	US-09-902-540-1098	Sequence 1098, Ap
C 44	97	8.7	2021	4	US-09-949-016-5379	Sequence 5379, Ap
C 45	97	8.7	2022	3	US-08-687-691B-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-620-312D-670  
Sequence 670, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunru  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radjoje T.  
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PL\_Fl\_genes Version 1.0  
SEQ ID NO 670  
LENGTH: 772  
TYPE: DNA

ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (24)..(665)  
 US-09-620-312D-670

## Alignment Scores:

Pred. No.:	1,07e-121	Length:	772
Score:	1118.00	Matches:	213
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-525-867-1 (1-213) x US-09-620-312D-670 (1-772)

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QY      1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgGlyLeuGlyLeuArgSerSer 20
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QY      21 ValGlyProAlaValAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
DB      84 GTGGGCGCGCTGTGACAGGACAGGTGTCATCAGAGCGTGGCCACCGATGGCCCAAGC 143
QY      41 SerThrGlnProAlaLeuProGlyAlaArgAlaValAlaProGlyProSerSerArgGly 60
DB      144 AGCACCCAGCGCTGCGCTGCGCAAGCCAGAGCCGTGGCTCCCAACCCAGCAGCCGGGGC 203
QY      61 GluTyrValValAlaAlaValLeuAspAspLeuValAsnTTPAlaArgSerSerLeuTTP 80
DB      204 GAGATATGTGTGCGCAAGCTGATGATCTGTCATCTGGGCGCGCGGAGTTCTCTGG 263
QY      81 ProMetThrPheGlyLeuAlaCysCysAlaValAlaGluMetMetHisMetAlaAlaProArg 100
DB      264 CCCATGACCTTGGCGCTGCGCTGCTGCGCGCTGAGATATGCAATGACAGCAGCCCGC 323
QY      101 TyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSerAspValMet 120
DB      324 TACGACATGACCGCTTTGGCGGTGCTTCCGCGCAGCCGCGCACTCCGACGTCAATG 383
QY      121 IleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValTyrAspGln 140
DB      384 ATCGTGGCGGACACTCACCACCAAGATGGCCCGAGCGCTTCGCAAGGTCAACAGCAG 443
QY      141 MetProGlnProArgTyrValValSerMetGlySerCysAlaAsnGlyGlyTyrTyr 160
DB      444 ATGCGGAGCCGCGCTACGTGCTCCATGGGAGCTGCGCAACGAGAGGGCTACTAC 503
QY      161 HisTyrSerTyrSerValValArgGlyCysAspArgIleValProValAspIleTyrIle 180
DB      504 CACTATTCCTACTCGGTGTGTGAGGGGCTGCGACGCAATCGGCCCGTGGACATCTACATC 563
QY      181 ProGlyCysProProThrAlaGlnAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgLys 200
DB      564 CCAGGCTCCCAACCTACCGGCGGAGCCCTGCTCAAGGCATCTCGACGCTGCAGAGAGAG 623
QY      201 IleLysArgGlyLysArgLysLeuGlnIleTyrTyrArg 213
DB      624 ATCAAGCGGAGCGGAGCGGAGCTGCAATCTGTACCGCAGG 662

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## RESULT 2

US-09-270-767-14895  
 Sequence 14895, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 APPLICANT: Homburger et al.  
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 FILE REFERENCE: File Reference: 7326-094  
 CURRENT APPLICATION NUMBER: US/09/270,767  
 NUMBER OF SEQ ID NOS: 62517  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 14895

LENGTH: 2378  
 TYPE: DNA  
 ORGANISM: *Drosophila melanogaster*  
 US-09-270-767-14895

## Alignment Scores:

Pred. No.:	1,68e-78	Length:	2378
Score:	756.50	Matches:	141
Percent Similarity:	83.76%	Conservative:	24
Best Local Similarity:	71.57%	Mismatches:	26
Query Match:	67.67%	Indels:	6
DB:	4	Gaps:	2

US-09-525-867-1 (1-213) x US-09-270-767-14895 (1-2378)

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QY      18 ArgSerSerValGlyProAlaValAlaArgGlyValHisGlnSerValAlaThrAsp 37
DB      1235 CGCTCTGAATTGGCCCTGGT-----GGCCCAACCAACCCCTTCAGTTGCCGAAGT 1288
QY      38 GlyProSerSerThrGlnProAlaLeuProGlyAlaArgAlaValAlaProGlyProSe 57
DB      1289 GGCACCAAAATCTGCCAAGAGGGCTA-----CTCTCCGTTCCGGCACCAACAGCT 1339
QY      57 rSerArgGlyGluTyrValValAlaAlaLysLeuAspAspLeuValAsnTTPAlaArgSe 77
DB      1340 CTCGCTTGGCGAGTGTCTCACTGGCCAGACCTGACGATCTGCTCACTGGGGTCCGAAGG 1399
QY      77 rSerLeuTTPProMetThrPheGlyLeuAlaCysCysAlaValAlaGluMetMetHisMetAl 97
DB      1400 CTGATCTGGCCCACTGACTTTGGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1459
QY      97 aaLAspAspGlyTyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSe 117
DB      1460 TGCTCCGCTTACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1519
QY      117 rAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVa 137
DB      1520 CGATGTCATCATCGTGTGCGTGGACCGCTGACCAACCAATGGCACCGGCTTGGCAAGGT 1579
QY      137 TyrAspGlnMetProGluProArgTyrValValSerMetGlySerCysAlaAsnGlyGly 157
DB      1580 CTACGACCAAAATGCGCGGACCGTGGATCATCTCATGAGGAGCGTGCACACCGCGG 1639
QY      157 yGlyTyrTyrHisTyrSerTyrSerValValaArgGlyCysAspArgIleValProValAs 177
DB      1640 CGGCTACTACCATTAATCTGTAATCGGTTCGTTGCGGCGGAGGCGCTCATGTACGGCGTTTGCAGCT 1699
QY      177 PileTyrIleProGlyCysProProThrAlaGlnAlaLeuLeuTyrGlyIleLeuGlnLe 197
DB      1700 CATATACGTACCCCGTTGTCCGCAACCGCGGAGGCGCTCATGTACGGCGTTTGCAGCT 1759
QY      197 uGlnArgLysIleLysArgGlyLysArgLysLeuGlnIleTyrTyrArg 213
DB      1760 GCAGAAGAAGATTAAAGGATGAAGACGCTCCAGATGTGTATGAAG 1808

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## RESULT 3

US-09-248-796A-2829  
 Sequence 2829, Application US/09248796A  
 Patent No. 6747137  
 GENERAL INFORMATION:  
 APPLICANT: Keith Weinstock et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 FILE REFERENCE: 107196.132  
 CURRENT APPLICATION NUMBER: US/09/248,796A  
 PRIOR FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 2829  
 LENGTH: 615



OTHER INFORMATION: H37RV  
US-09-103-840A-1

Alignment Scores:  
Pred. No.: 1,996-37  
Score: 449.00  
Percent Similarity: 60.918  
Best Local Similarity: 41.828  
Query Match: 40.164  
Length: 4411529  
Matches: 92  
Conservative: 42  
Mismatch: 38  
Indels: 48  
Gaps: 6

US-09-525-867-1 (1-213) x US-09-103-840A-1 (1-4411529)

```

QY 4 LeuSerAlaProGlyLeuArgGlyPheArgIle-----Leu 15
DB 3511999 ATTCATGCTCACGCGTGTGCTGCTACGCTATGCTGCGCGCGCGGCGCTGACCTG 3512058
QY 16 GlyLeuArgSerSerValGlyProAlaValGlnAlaArgGlyValHisGlnSerValAla 35
DB 3512059 GGATTGAGGTAGGGGGTGGG----- 3512079
QY 36 ThrAspGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys 55
DB 3512080 -----CTGGAGAAACAGCTGCC----- 3512097
QY 56 ProSerSerArgGlyGlyIuTyValValAlaLysLeuAspAspLeuValAsnTrpAlaArg 75
DB 3512098 -----GGCGGATCTGCTGCTGCTGCGAGAGAGGTGGCGGCTATGTCGCG 3512145
QY 76 ArgSerSerLeuTrpProMetThrPheGlyLeuAlaCysCysAlaValGlnMetMetHis 95
DB 3512146 AAAAAGCTCCGTGGCGCGGCGGACATTCGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCG 3512205
QY 96 MetAlaAlaProArgTrpArgMetAspArgPheGlyValVal-----PheArgAlaSerPro 114
DB 3512206 ACCGCGGAGCAAGAGTTTGACATGCGCGGCTTGGGATGGAACGGCTTCTCGGCGCGCG 3512265
QY 115 ArgGlnSerAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeu 134
DB 3512266 CGGAGGAGGAGATCTGATGATGCTGCGCGCGCGGCTGACGACAGATGCGCGCGGCTGACTG 3512325
QY 135 ArgLysValTyAspGlnMetProGluProArgTrpValValSerMetGlySerCysAla 154
DB 3512326 CGCAGATCTATGACCAAGATGCGGAGCGGAAATGGTTCTGCGCATGCGGTGTGCGCC 3512385
QY 155 AsnGlyGlyGlyTyTrpHisTySerTySerValValaArgGlyCysAspArgIleVal 174
DB 3512386 TCGTCAAGTGGGATGTTCAAC---AATATGCGATCGTGCAGCGCGCTGATCATGTGTT 3512442
QY 175 ProValAspIleTyTrpHisTySerTySerProProThrAlaGlnAlaLeuLeuTyGlyIle 194
DB 3512443 CCGGTGCAATCTTACCTTACCTGCGCGCGCGCGCGCGCGGAGATGCTGTCGACGCGCATC 3512502
QY 195 LeuGlnLeuGlnArgLysIleLys-----ArgGluArgGluLeu 207
DB 3512503 CTGAAGCTGCAGCAAAAGATTACGACAGATGCCATTAGTATCAACCGGAGCAACGCTATC 3512562

RESULT 6
US-09-252-991A-14622/c
; Sequence 14622 Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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SEQ ID NO 14622  
LENGTH: 966  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14622

Alignment Scores:  
Pred. No.: 6,356-42  
Score: 440.00  
Percent Similarity: 59.03%  
Best Local Similarity: 43.17%  
Query Match: 39.36%  
Length: 966  
Matches: 98  
Conservative: 36  
Mismatch: 61  
Indels: 32  
Gaps: 7

US-09-525-867-1 (1-213) x US-09-252-991A-14622 (1-966)

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QY 12 PheArgIleLeuGlyLeuArgSerSerValGlyProAlaValGlnAlaArgGlyValHis 31
DB 951 TGGCGGCTCTTG-----TCTATCTTGGCGGATCGTGCCTGATGCGGCTCGCG 901
QY 32 GlnSerValAlaThrAspGlyProSerSerThrGlnProAlaLeu----- 46
DB 900 AAAGCCGTCCCAAGCGCGGCGGCAAGCTTAAACAATGAGCTTTGCGATGCATACAA 841
QY 47 -----ProLysAla-----ArgAlaVal 52
DB 840 CTTACCCGATCGATCCGATCGCGCAACGCAATACCGGATGCGGAAACGGGAAAC 781
QY 53 AlaProLysProSerSerArgGlyGlu-----TyValValAlaLysLeuAsp 68
DB 780 GTACCGGACCGGTGTGAGGCGGCGGAGGCTGACAGAAACATCTTCATGCGGACCTGAG 721
QY 69 AspLeu-----ValAsnTrpAlaArgArgSerSerLeuTrpProMetThrPhe 84
DB 720 GATGCTGCACTCCACCGTCAACGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 661
QY 85 GlyLeuAlaCysCysAlaValaGlnMetMetHisMetAlaAlaProArgTyAspMetAsp 104
DB 660 GCGCTGTGCTGTGCTGTAGTGAATGACCAACCGCTTACCGCGCGGCGGCGGCGGCGGCGG 601
QY 105 ArgPheGlyVal-----ValPheArgAlaSerProArgGlnSerAspValMetIleValAla 123
DB 600 CCGTTCGCGCGGCGGAGTATCCGCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541
QY 124 GlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValTyTrpHisTySer 143
DB 540 GGCACCTGCTTCATCAAGATGCGCGCGGCTGATCAGAGGCGCTTACGACGAGATGCTCGAA 481
QY 144 ProArgTyValValSerMetGlySerCysAlaAsnGlyGlyTyTrpHisTySer 163
DB 480 CCAAGTGGGTATCTCATGAGGCTGCTGCGCAATTCGCGGCGGCGGCGGCGGCGGCGGCGG 424
QY 164 TySerValValaArgGlyCysAspArgIleValProValAspIleTyTrpProGlyCys 183
DB 423 TATTCGTGTTCACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364
QY 184 ProProThrAlaGlnAlaLeuLeuTyGlyIleLeuGlnLeuGlnArgLysIleTyArg 203
DB 363 CCGCGCGGCGGCGGAGGCGGCTTCTGCAAGGCTTGAATGCTTTCAGGAATTCATCGGCGAG 304
QY 204 GluArgArgLeuGlnLeuTrp 210
DB 303 GAGCGCGCGCGGCTGCTG 283

RESULT 7
US-09-489-039A-5374
; Sequence 5374 Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001

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;; CURRENT APPLICATION NUMBER: US/09/489,039A  
;; CURRENT FILING DATE: 2000-01-27  
;; PRIOR APPLICATION NUMBER: US 60/117,747  
;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 14342  
;; SEQ ID NO 5374  
;; LENGTH: 690  
;; TYPE: DNA  
;; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5374

Alignment Scores:  
Pred. No.: 1,12e-41 Length: 690  
Score: 436.00 Matches: 79  
Percent Similarity: 73.10% Conservative: 27  
Best Local Similarity: 54.48% Mismatches: 37  
Query Match: 39.00% Indels: 2  
DB: Gaps: 2

US-09-525-867-1 (1-213) x US-09-489-039A-5374 (1-690)

QY 67 LeuaphleuValaentTrralaArgSerSerLeuTrrPrometThPhgIyleu 86  
DB 151 CTGCATGACATGTAAGCTGGGCGGTAAAGTCAATTTGGCCGTACACCTTGGCCTT 210  
QY 87 AlaCyseCybaValaGluMetMetHleMetAlaAlaProArgTyrAspMetAspArgPhe 106  
DB 211 TCTTCTCTTATGTGGAATGTGACATTCATTCATCGCGGTGACATGACGCTTTT 270  
QY 107 GlyVal---ValPheArgAlaSerProArgInSerAspValMetIleValaIaGlyThr 125  
DB 271 GGGGCAAGAGTTCTGGCGGCTCTCCGCGTACGCGGACCTGATGCTGGCGGAACC 330  
QY 126 LeuThrAnlyMetAlaProAlaLeuArglyValTyrAspGlnMetProGluProArg 145  
DB 331 TGCCTTACCAAAATGGCGCCGTTATTCAGCGTCTACGATCAGATCTGAGCCGAAAG 390  
QY 146 TyrValaIaSerMetGlySerCybaIaAsnGlyGlyTyrTyrHisTyrSerTyrSer 165  
DB 391 TGGGTATCTTCATGGGCGCTGGCCCACTCAGCGGGAGATGACATC---TATTCC 447  
QY 166 ValValaIaArgGlyCybaAspArgIleValaProValaAspIleTyrIleProGlyCybaPro 185  
DB 448 GTCTCCAGGGCGTGAATTAATTCATTCGCGTGTGATGATCCCGGCTGCGCGCG 507  
QY 186 ThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArglyIleValaArgGlyArg 205  
DB 508 CGTCCGAGGCGCTATATGACAGCGCTGCTGTGACAGAGTCCATTGTAAAGACGT 567  
QY 206 ArgLeuGlnIleTrrp 210  
DB 568 CGTCCGCTCTCATGG 582

RESULT 8  
US-09-252-991A-15142  
; Sequence 15142, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15142  
; LENGTH: 696  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-15142

Alignment Scores:  
Pred. No.: 1,14e-41 Length: 696  
Score: 436.00 Matches: 86  
Percent Similarity: 69.88% Conservative: 30  
Best Local Similarity: 51.81% Mismatches: 39  
Query Match: 39.00% Indels: 11  
DB: Gaps: 4

US-09-525-867-1 (1-213) x US-09-252-991A-15142 (1-696)

QY 55 LysProSerSerArgGly-----GluTyrVal-ValaIaLysLeuAspArgPhe 70  
DB 96 CGACCCCGGTGATCAGAGGCCAGGTTCACAGAACATCTTCATGGAGCAAGCTCGAGAGATG 155  
QY 70 u-----ValaentTrralaArgSerSerLeuTrrPrometThPhgIyle 86  
DB 156 GCTGAACCTCACCCCTCACTGGGGTGCAGAACCTCGCTGCGCTTAACTTCGGGCT 215  
QY 86 uAlaCyseCybaValaGluMetMetHleMetAlaAlaProArgTyrAspMetAspArgPhe 106  
DB 216 GTCTGCTCTACGTGAGATGACACCGCTTCACCGCGCCGACGATATCGCCGCTT 275  
QY 106 eGlyVal---ValPheArgAlaSerProArgInSerAspValMetIleValaIaGlyThr 125  
DB 276 CGGCGCGAAGTATCCGGGGGTGCGCGCGGACGAGCGACTTCATGTCATGCGCGGAC 335  
QY 125 rLeuThrAnlyMetAlaProAlaLeuArglyValTyrAspGlnMetProGluProArg 145  
DB 336 CTGCTTCATCAAGATGCGCCGCGTATCCACCGCTTCACAGAGATGTCGAACCGAA 395  
QY 145 gTyrValaIaSerMetGlySerCybaIaAsnGlyGlyTyrTyrHisTyrSerTyrSer 165  
DB 396 GTGGTATCTTCATGGGCTCTGCGCCCAATTCGCGCGGACATGACATC---TATTCC 452  
QY 165 rValaIaArgGlyCybaAspArgIleValaProValaAspIleTyrIleProGlyCybaPro 185  
DB 453 GTGTGTCCAGGGGTGCAAGATTCCTCCCGTGGAGCTTACATCCCGGCTGCGCGCC 512  
QY 185 oThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArglyIleValaArgGlyArg 205  
DB 513 CGTCCGAGGCGTCTCTGCAAGGCTGATGCTGTGACAGAAATTCATCGGCGAGAGCG 572  
QY 205 ArgLeuGlnIleTrrp 210  
DB 573 CGGCGCGCTGCTGG 588

RESULT 9  
US-09-543-681A-43  
; Sequence 43, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 43  
; LENGTH: 735  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-43

Alignment Scores:  
Pred. No.: 2,78e-41 Length: 735  
Score: 433.00 Matches: 80  
Percent Similarity: 72.41% Conservative: 25  
Best Local Similarity: 55.17% Mismatches: 38

Query Match: 38.73% Indels: 2  
DB: 4 Gaps: 2

US-09-525-867-1 (1-213) x US-09-543-681A-43 (1-735)

QY 67 LeuAspAspLeuValAsnTrpAlaArgArgSerLeuTrpProMetThrPheGlyLeu 86  
DB 196 TTAACATGACGTGTGTAAGCTGGGAGCAAAAACTCTTAATGGCCATTAATATTGGTCTT 255  
QY 87 AlaCyCyAlaValAlaGlnMetMetHisMetAlaAlaProArgTrpAspMetAspArgphe 106  
DB 256 TCCCTGTTGTTACGTGTAATGGTGAAGCTCATTTACTGCGGTCAGTGAAGCTGAGCCGTTT 315  
QY 107 Gly---ValValPheArgAlaSerProArgGlnSerAspValMetCileValAlaGlyThr 125  
DB 316 GATTCTGAAGATTAACGCTTCCCTCGTCAAGCTGACTTAAAGGCTTGAAGGAGCAAGACC 375  
QY 126 LeuThrAsnLysMetAlaProAlaLeuArgLysValTrpAspGlnMetProGluProArg 145  
DB 376 TGCTTTACAAAGATGCGCCCGCTTAATTCAGCGTTTAACATCATGATGATGAGCCTAAG 435  
QY 146 TyrValValSerMetGlySerCyAlaAsnGlyGlyTrpTrpHisTrpSerTrpSer 165  
DB 436 TGGGTATTTTCCATGAGGAGCTTGGCTAATCTGCTGATGATGATGATGATGATGATGATG 492  
QY 166 ValValArgGlyCysAspArgLysValProValAspLysTrpLeuProGlyCysProPro 185  
DB 493 GTACTGCAAGGTGTGTAATTAATTCATTCCTGTTGATGTGTAATCCAGAGATGCCACCT 552  
QY 186 ThrValaGlnAlaLeuLeuTrpGlyLysLeuGlnArgLysLysArgGlyArg 205  
DB 553 CGTCCAAAGCTTAATATGCAAGCATTGATGTTATTAAGAGATCCATTGTTAAAGACGT 612  
QY 206 ArgLeuGlnLysLeuTrp 210  
DB 613 CGCCCATTAATCTTG 627

RESULT 10  
US-09-596-002-30  
/ Sequence 30, Application US/09596002  
/ Patent No. 6632636  
/ GENERAL INFORMATION:  
/ APPLICANT: Lagace, Robert, E.  
/ APPLICANT: Patterson, Chandra  
/ APPLICANT: Berg, Kim, L.  
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
/ FILE REFERENCE: PM-0008-4 US  
/ CURRENT APPLICATION NUMBER: US/09/596,002  
/ PRIOR FILING DATE: 2000-06-16  
/ PRIOR APPLICATION NUMBER: 60/140,121  
/ NUMBER OF SEQ ID NOS: 1999-06-18  
/ SOFTWARE: PERL Program  
/ SEQ ID NO 30  
/ LENGTH: 58909  
/ TYPE: DNA  
/ ORGANISM: M. catarrhalis  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Incyte template ID No. 6632636 30  
/ PUBLICATION INFORMATION:  
US-09-596-002-30

Alignment Scores:  
Pred. No.: 3,246-38 Length: 58909  
Score: 431.50 Matches: 88  
Percent Similarity: 67.05% Conservative: 30  
Best Local Similarity: 50.00% Mismatches: 52  
Query Match: 38.60% Indels: 7  
Gaps: 3

US-09-525-867-1 (1-213) x US-09-596-002-30 (1-58909)

QY 36 ThrAspGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys 55  
DB 26810 ACCAACATATCCAAAGCAATCCACAAACAAACCGGTGAATCATTTAGAGATATCCACAG 26869  
QY 56 ProSerSerArgGlyGlyTrpValValAlaLysLeuAspSer-----LeuVal 71  
DB 26870 CCGAGGTG-GATTAATAAGCTTTTGGGAGATTTGCCAATTTGACGCAACACTTGGCC 26928  
QY 72 AsnTrpAlaArgArgSerSerLeuTrpProMetThrPheGlyLeuAlaCyCyAlaVal 91  
DB 26929 AACTGGGGTGCACAAACCTCTTAATGCGCTTTAACTTTGGCAGCAAGCTGTTTATGTC 26988  
QY 92 GlnMetMetHisMetAlaAlaProArgTrpAspMetAspArgPheGlyVal---ValPhe 110  
DB 26989 GAGTATGCGACGACCTTGACAGGCGTGCATGATTTGCTGTTTGGGCGAGAGCTCAT 27048  
QY 111 ArgAlaSerProArgGlnSerAspValMetCileValAlaGlyThrLeuThrAsnLysMet 130  
DB 27049 CGTCCCTCCCTCGCCAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 27108  
QY 131 AlaProAlaLeuArgLysValTrpAspGlnMetProGluProArgTrpValValSerMet 150  
DB 27109 GCGCTGTGATTTCTCAGGCTGATGACAAATGTTAAGAACTTAATGGGTCAATCTCCATG 27168  
QY 151 GlySerCyAlaAsnGlyGlyTrpTrpHisTrpSerTrpSerValValArgLysCys 170  
DB 27169 GGGGCGGTGCCAACTCTGTGTCATGTCAGCATTT---TATTCGTGTCAGAGGGGTG 27225  
QY 171 AspArgLysValProValAspLysTrpLeuProGlyCysProProThrAlaGlnAlaLeu 190  
DB 27226 GATTAATCTTGGCTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 27285  
QY 191 LeuTrpGlyLysLeuGlnLysArgLysLysArgGlyArg 206  
DB 27286 ATTCAAGCATCATGCTATTAAGAGAGCATTTCAAAAGAACCCCGT 27333

RESULT 11  
US-09-790-988-1  
/ Sequence 1, Application US/0790988  
/ Patent No. 6632935  
/ GENERAL INFORMATION:  
/ APPLICANT: SHIGENOBU, SHUJI  
/ APPLICANT: WATANABE, HIDEKI  
/ APPLICANT: HATTORI, MASAHIRA  
/ APPLICANT: SAKAKI, YOSHIYUKI  
/ TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
/ FILE REFERENCE: 081356/0159  
/ CURRENT APPLICATION NUMBER: US/09/790,988  
/ PRIOR FILING DATE: 2001-02-23  
/ CURRENT APPLICATION NUMBER: JP2000-107160  
/ PRIOR FILING DATE: 2000-04-07  
/ NUMBER OF SEQ ID NOS: 7  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 1  
/ LENGTH: 640681  
/ TYPE: DNA  
/ ORGANISM: Buchnera sp.  
US-09-790-988-1

Alignment Scores:  
Pred. No.: 3,126-36 Length: 640681  
Score: 428.00 Matches: 81  
Percent Similarity: 72.41% Conservative: 24  
Best Local Similarity: 55.86% Mismatches: 38  
Query Match: 38.28% Indels: 2  
Gaps: 2

US-09-525-867-1 (1-213) x US-09-790-988-1 (1-640681)

QY 67 LeuAspAspLeuValAsnTrpAlaArgArgSerLeuTrpProMetThrPheGlyLeu 86  
DB 165027 TTAACATTAATTAATTAATTTGGGTCGAAAAAATCTTAATGCTTAATTAATTTGGTCTG 165086





DB 472 TAGTCCAGGTTGCTCGCTCGTAGAGATTATCAAGATTAAAGCTTTTACAA 531  
QY 199 ATGlyS11eLyArGluArGArg 206  
DB 532 GACCAAGATTCAATTAGAGCGACG 555

RESULT 14  
US-09-020-956-32/c  
Sequence 32, Application US/09020956  
Patent No. 6261562  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,956  
FILING DATE: 09-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-020-956-32

Alignment Scores:  
Pred. No.: 1,19e-38 Length: 789  
Score: 411.00 Matches: 114  
Percent Similarity: 62.11% Conservative: 4  
Best Local Similarity: 60.00% Mismatches: 54  
Query Match: 36.76% Indels: 21  
DB: 3 Gaps: 2

US-09-525-867-1 (1-213) x US-09-020-956-32 (1-789)

QY 36 ThrspglYProSerSerThnGlnProAlaLeuProLySAlaArgAlaValAlaProLyS 55  
DB 696 ACCGGGGGCCCGAAGGGGGGAGCANNCTTGGCCNNCCAAAGNNAGAGCGCGGTTCCCAAA 637  
QY 56 ProSerSerArGlyGlyUryrValAlaAlaLlyLeuAspSP-LeuValAsnTrpAlaAr 75  
DB 636 CCCAGNANAGCGGGGAGGATTTGGGGGCCCAAGGGGATGACTTGTGTG----- 588  
QY 75 gArGSerSerLeuTrpPro-----MetThrPhgGlyLeuAl 87  
DB 587 -----AAACTGGGNCCTCCCGAGNTTTTGGNGGCCNCAAGAACTTTGGGTGAC 535  
QY 87 aCySAlaValAlaGluMetMetAlaAla-ProArGTrYrAspMetLaSpArGpHe- 106  
DB 534 CTGTGNGCCCGGGAGGTGATGNANATNGCAGCAACCCGNNAGACATGNCCTGTTT 475

QY 107 -GlyValValPheArgAlaSerProArgGlnSerAspValMetLleValAlaGlyThrLe 126  
DB 474 GGGGNGNTTTTGGGGCCAGCCGAGCTCTGA-GTANATGATTGGCGNANANT 416  
QY 126 UThrAsnLySMeAlaProAlaLeuArGlyValTrYrAspG1MeCProG1UpPoArGTY 146  
DB 415 AACCAAAAAGAGGGCCAGNGTTGC-ANGTTTAAGACCAATGCCAGGCCGAGANA 357  
QY 146 rValValSerMetGlySerCySAlaAngLyGlyTrYrTrh1STySerTySerya 166  
DB 356 AGTGTTTCCANGGGAGTGN-GCCAACGAGNGGGGTANACCACATATTCTAATNGT 298  
QY 166 lValArg1YCySAspArg1LeValProValAsp1LeTy1LeProG1YCySProth 186  
DB 297 GGTAGGGGNTGCCAGCGCATTTGCCCGGGAATTAATCCAGGGTGCCACCNAN 238  
QY 186 rAlaGluAlaLeuLeuTrYrGly1LleuGlnLeuGlnArGlyS1LlySaArg1UArGAr 206  
DB 237 GCGCAGGCCCCGTGTTTANGCATCCTGCAGCTGCAGAGAGANATCAAGCGGAGCGAG 178  
QY 206 gLeuGln1LeTrpTrYrArGArg 213  
DB 177 GCTCANATTGGTACCGCAGG 156

RESULT 15  
US-09-030-607-32/c  
Sequence 32, Application US/09030607  
Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-030-607-32

Alignment Scores:  
Pred. No.: 1,19e-38 Length: 789  
Score: 411.00 Matches: 114  
Percent Similarity: 62.11% Conservative: 4  
Best Local Similarity: 60.00% Mismatches: 54  
Query Match: 36.76% Indels: 21  
DB: 3 Gaps: 2

US-09-525-867-1 (1-213) x US-09-030-607-32 (1-789)

Qy	36	ThrAspG1ProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys	55
Db	696	ACCGGGGGGGCCGAAGGGGGAGCANCCTGGCCNCCAAAGGAGGCGGTGCCAAA	6377
Qy	56	ProSerSerArgG1yG1uTrValAlaAlaLysLeuAspAspLeuValSerTrpAlaAr	75
Db	636	CCCAAGNAACGGGGGGAGGATTTGGGGGCGAAGGGGATGACTTTGTG-----	588
Qy	75	gArGSerSerLeuTrpPro-----MetThrPheG1yLeuAl	87
Db	587	-----AACTGGGNGCCCCCGAGNTTTTTTNGGGCCNCAAGAACTTTGGGTTGNC	535
Qy	87	aCySyaAlaValaGlnMetMetHisMetAlaAla-ProArgTrpAspMetAspRhe-	106
Db	534	CTGNTNGGCCCCGGAGGTGATGNAATNGCAAGCAACCCGAGNAAGACTGGCCGGTTTT	475
Qy	107	-G1yAlaValaPheArgAlaSerProArgGlnSerAspValMetIleValaLag1TrIe	126
Db	474	GGGNGNTTTTTTGGGGCCAGCCCGNGCAGCTGA-CTNATGATTTGGCGNGNAAANT	416
Qy	126	uThraenLybMetAlaProAlaLeuArgLyValaTyraSpGlnMetProGluProArgTy	146
Db	415	AACCAAAAAGAGGCCCCCGANGTTTGC-AAGGTTTAAAGACAGATGCGGAGCCGCGANA	357
Qy	146	rValaValaSerMetGlySerCyAlaAspG1yG1yLyTrpTrpHisTrpSerTrsVal	166
Db	356	AGGGTTCCTCAGGGGAGTGN-GCCAACGGNGNGGTAAANACCACTATTCCTAATNGT	298
Qy	166	1ValaTrG1yCybAspArgIleValProValaAspIleTyrlleProG1yCybProTh	186
Db	297	GGTGAAGGNGTGGACCGCATTTGTCCCTGTGAATTTAAATTCACAGGTGCCACCNAN	238
Qy	186	rAlaG1uaLeuLeuTyrg1yTlLeuGlnLeuGlnArgLyS1leYsaG1uaArg	206
Db	237	GGCGGAGGCCCTGTTTANGGATCTCTGACGCTGCAGAGAAATTCACGCGAGCGAG	178
Qy	206	gLeuGlnIleTrpTyraArg	213
Db	177	GCTGCANATTTGGTACCGCAGG	156

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 00:37:15 ; Search time 2937 Seconds  
(without alignments)  
1670.227 Million csl1 updates/sec

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Perfect score: 824  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750.8	91.1	772	US-10-037-270-670	Sequence 670, App
2	750.8	91.1	772	US-10-117-722-670	Sequence 670, App
3	569.2	59.1	2818	US-10-104-047-825	Sequence 625, App
4	491	59.6	3050	US-10-104-047-262	Sequence 262, App
5	427.2	51.8	3089	US-10-104-047-914	Sequence 914, App
6	384.6	46.7	789	US-09-759-143-32	Sequence 32, App1
7	384.6	46.7	789	US-09-780-668-32	Sequence 32, App1
8	384.6	46.7	789	US-09-030-606-32	Sequence 32, App1
9	384.6	46.7	789	US-09-822-827-32	Sequence 32, App1
10	384.6	46.7	789	US-09-115-453-32	Sequence 32, App1
11	384.6	46.7	789	US-09-233-880-32	Sequence 32, App1

c 12	384.6	46.7	789	9	US-09-895-793-32	Sequence 32, App1
c 13	384.6	46.7	789	9	US-09-895-814-32	Sequence 32, App1
c 14	384.6	46.7	789	13	US-10-012-896-32	Sequence 32, App1
c 15	384.6	46.7	789	14	US-10-010-840-32	Sequence 32, App1
c 16	384.6	46.7	789	16	US-10-144-678A-32	Sequence 32, App1
c 17	384.6	46.7	789	16	US-10-294-025-32	Sequence 32, App1
c 18	384.6	46.7	789	16	US-10-688-838-32	Sequence 55, App1
c 19	344	41.7	344	18	US-10-775-169-55	Sequence 195, App1
c 20	307.4	37.3	466	17	US-10-152-119A-195	Sequence 92496, A
c 21	300.2	36.4	1142	18	US-10-437-863-92496	Sequence 36399, A
c 22	279.2	33.9	863	17	US-10-425-114-36399	Sequence 14502, A
c 23	278.6	33.8	1092	18	US-10-767-701-14502	Sequence 3675, Ap
c 24	278.6	33.8	1840	18	US-10-425-115-3875	Sequence 16284, A
c 25	277.6	33.7	886	17	US-10-425-114-16284	Sequence 6711, A
c 26	277.6	33.7	949	17	US-10-425-115-3877	Sequence 3877, Ap
c 27	277.6	33.7	1394	18	US-10-425-115-3877	Sequence 6217, Ap
c 28	269.8	32.7	1532	17	US-10-424-599-6217	Sequence 6216, Ap
c 29	266.6	32.4	1356	17	US-10-424-599-6216	Sequence 2049, Ap
c 30	260.8	31.7	753	17	US-10-320-797-2049	Sequence 158531, A
c 31	257	31.2	274	18	US-10-425-115-158531	Sequence 18993, A
c 32	254.6	30.9	797	18	US-10-767-701-19893	Sequence 7030, Ap
c 33	233	28.3	2731748	18	US-10-297-465A-1	Sequence 715, App
c 34	221.6	26.9	735	15	US-10-128-714-7030	Sequence 715, App
c 35	190	23.1	2179	17	US-10-094-749-715	Sequence 316, App
c 36	190	23.1	3743	17	US-10-104-047-273	Sequence 4866, Ap
c 37	190	23.1	34875	18	US-10-775-169-316	Sequence 1, App1
c 38	184.4	22.4	609	15	US-10-156-761-4866	Sequence 2030, Ap
c 39	184.4	22.4	9025608	15	US-10-128-714-2030	Sequence 1030, Ap
c 40	183.8	22.3	570	15	US-10-128-714-1030	Sequence 6030, Ap
c 41	183.8	22.3	596	15	US-10-128-714-6030	Sequence 30, App1
c 42	183.8	22.3	873	15	US-10-128-714-30	Sequence 5030, Ap
c 43	183.8	22.3	2596	15	US-10-128-714-5030	Sequence 4822, Ap
c 44	183.8	22.3	2873	15	US-10-128-714-5030	
c 45	177	21.5	552	15	US-10-156-761-4822	

#### ALIGNMENTS

RESULT 1  
US-10-037-270-670  
; Sequence 670, Application US/10037270  
; Publication No. US20030104529A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Aseundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aildong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yundong  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhimei  
; APPLICANT: Tillinghast, John  
; APPLICANT: Dirmacac, Radoje T.  
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/10/037, 270  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pc\_fl\_genes Version 1.0  
; SEQ ID NO 670

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; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24)..(665)
US-10-037-270-670
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Query Match      91.1%; Score 750.8; DB 15; Length 772;
Best Local Similarity 99.1%; Pred. No. 3.7e-199;
Matches 755; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 63 GAAGCCGAGGCGCAAGATGCGCTGTGTCACTCTCTGCGCGGCTTCCGATCCT 122
Db 8 GAAGCCGAGGCGCAAGATGCGCTGTGTCACTCTCTGCGCGGCTTCCGATCCT 67
QY 123 TGGTCTGCGCTTCAAGCGTGGCCCGGCTGTGAAGCAAGAGTGTCCATCAAGAGTGGC 182
Db 68 TGGTCTGCGCTTCAAGCGTGGCCCGGCTGTGAAGCAAGAGTGTCCATCAAGAGTGGC 127
QY 183 CACCGATGGCCCAAGCAGACACCCAGCTGTGCTTCCAAAGGCCAGAGCCGTGGCTCCAA 242
Db 128 CACCGATGGCCCAAGCAGACACCCAGCTGTGCTTCCAAAGGCCAGAGCCGTGGCTCCAA 187
QY 243 ACCGAGCAGCCGGGGCGAGTATGTGTGGCAAGCTGGATGACTGTCACTGGGCTCCG 302
Db 188 ACCGAGCAGCCGGGGCGAGTATGTGTGGCAAGCTGGATGACTGTCACTGGGCTCCG 247
QY 303 CCGGAGTTCTGTGGGCCCATGACCTTGGGCTGTGGCTGTGGCGCGTGAAGATATGCA 362
Db 248 CCGGAGTTCTGTGGGCCCATGACCTTGGGCTGTGGCTGTGGCGCGTGAAGATATGCA 307
QY 363 CATGGCAGCACCCCGCTACGACATGACCGCTTGGGCGTGTCTTCCGCGCAGCCGCG 422
Db 308 CATGGCAGCACCCCGCTACGACATGACCGCTTGGGCGTGTCTTCCGCGCAGCCGCG 367
QY 423 CCAAGTCCAGGTATGATGTGGCCGCGCACTCACTCAACAAAGATGGCCCGGCTTCCG 482
Db 368 CCAAGTCCAGGTATGATGTGGCCGCGCACTCACTCAACAAAGATGGCCCGGCTTCCG 427
QY 483 CAAGGTCTACGACAGATGCGGAGCGGCTAAGGTCCTCAATGGGAGCTCCGCAA 542
Db 428 CAAGGTCTACGACAGATGCGGAGCGGCTAAGGTCCTCAATGGGAGCTCCGCAA 487
QY 543 CCGAGAGGCTACTACCACTATTCTACTCGGTGTGAAGGGCTGCGACCGCATCGTGC 602
Db 488 CCGAGAGGCTACTACCACTATTCTACTCGGTGTGAAGGGCTGCGACCGCATCGTGC 547
QY 603 CGTGAACATTCATCCAGGCTGCCACCTAAGCGGAGGCCCTGTCTTACCGCATCTT 662
Db 548 CGTGAACATTCATCCAGGCTGCCACCTAAGCGGAGGCCCTGTCTTACCGCATCTT 607
QY 663 GCAGCTGAGAGGAAGATCAAGCGGAGCGGAGCTGATCTGTATCCGACAGTATGAGG 722
Db 608 GCAGCTGAGAGGAAGATCAAGCGGAGCGGAGCTGATCTGTATCCGACAGTATGAGG 667
QY 723 CCGCGCCGCGCGCGCGGAGCGCTGTGCGGCTCTGTGCCCAAGCTGTGTGTCCGTTG 782
Db 668 CCGCGCCGCGCGCGCGGAGCGCTGTGCGGCTCTGTGCCCAAGCTGTGTGTCCGTTG 727
QY 783 AGGTGTCAATTAACCTGCGCTCGGCGCAAAAAA 824
Db 728 AGGTGTCAATTAACCTGCGCTCGGCGCAAAAAA 769
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RESULT 2  
US-10-117-722-670

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; Sequence 670, Application US/10117722
; Publication No. US2003021974A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aundt, Vinod
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; APPLICANT: Zhang, Jie
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US2003021974A1 Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc FL_genes Version 1.0
; SEQ ID NO 670_
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24)..(665)
US-10-117-722-670
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Query Match      91.1%; Score 750.8; DB 17; Length 772;
Best Local Similarity 99.1%; Pred. No. 3.7e-199;
Matches 755; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 63 GAAGCCGAGGCGCAAGATGCGGTGTGTCACTCTCTGCGCGGCTTCCGATCCT 122
Db 8 GAAGCCGAGGCGCAAGATGCGGTGTGTCACTCTCTGCGCGGCTTCCGATCCT 67
QY 123 TGGTCTGCGCTTCAAGCGTGGCCCGGCTGTGAAGCAAGAGTGTCCATCAAGAGTGGC 182
Db 68 TGGTCTGCGCTTCAAGCGTGGCCCGGCTGTGAAGCAAGAGTGTCCATCAAGAGTGGC 127
QY 183 CACCGATGGCCCAAGCAGACACCCAGCTGTGCTTCCAAAGGCCAGAGCCGTGGCTCCAA 242
Db 128 CACCGATGGCCCAAGCAGACACCCAGCTGTGCTTCCAAAGGCCAGAGCCGTGGCTCCAA 187
QY 243 ACCGAGCAGCCGGGGCGAGTATGTGTGGCAAGCTGGATGACTGTCACTGGGCTCCG 302
Db 188 ACCGAGCAGCCGGGGCGAGTATGTGTGGCAAGCTGGATGACTGTCACTGGGCTCCG 247
QY 303 CCGGAGTTCTGTGGGCCCATGACCTTGGGCTGTGGCTGTGGCGCGTGAAGATATGCA 362
Db 248 CCGGAGTTCTGTGGGCCCATGACCTTGGGCTGTGGCTGTGGCGCGTGAAGATATGCA 307
QY 363 CATGGCAGCACCCCGCTACGACATGACCGCTTGGGCGTGTCTTCCGCGCAGCCGCG 422
Db 308 CATGGCAGCACCCCGCTACGACATGACCGCTTGGGCGTGTCTTCCGCGCAGCCGCG 367
QY 423 CCAAGTCCAGGTATGATGTGGCCGCGCACTCACTCAACAAAGATGGCCCGGCTTCCG 482
Db 368 CCAAGTCCAGGTATGATGTGGCCGCGCACTCACTCAACAAAGATGGCCCGGCTTCCG 427
QY 483 CAAGGTCTACGACAGATGCGGAGCGGCTAAGGTCCTCAATGGGAGCTCCGCAA 542
Db 428 CAAGGTCTACGACAGATGCGGAGCGGCTAAGGTCCTCAATGGGAGCTCCGCAA 487
QY 543 CCGAGAGGCTACTACCACTATTCTACTCGGTGTGAAGGGCTGCGACCGCATCGTGC 602
Db 488 CCGAGAGGCTACTACCACTATTCTACTCGGTGTGAAGGGCTGCGACCGCATCGTGC 547
QY 603 CGTGAACATTCATCCAGGCTGCCACCTAAGCGGAGGCCCTGTCTTACCGCATCTT 662
Db 548 CGTGAACATTCATCCAGGCTGCCACCTAAGCGGAGGCCCTGTCTTACCGCATCTT 607
QY 663 GCAGCTGAGAGGAAGATCAAGCGGAGCGGAGCTGATCTGTATCCGACAGTATGAGG 722
Db 608 GCAGCTGAGAGGAAGATCAAGCGGAGCGGAGCTGATCTGTATCCGACAGTATGAGG 667
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Db 668 CCGCGCGCGCGCGCGCGCGAGCTGTCCGCTCTGTCCCGAGCCTGCTTGCTGCCGTG 727  
Qy 783 AGGTTGTAATAAAGCTTCCCTCGGGCAAAAAAAAAAAAAA 824  
Db 728 AGGTTGTAATAAAGCTTCCCTCGGGCTGGCGCCCAAAAAA 769

## RESULT 3

US-10-104-047-625  
; Sequence 625, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 625  
; LENGTH: 2818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-625

Query Match 69.1%; Score 569.2; DB 17; Length 2818;  
Best Local Similarity 97.8%; Pred. No. 1.4e-148;  
Matches 577; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 56 GTTGTCTGAAGGCGCGCGCGCGCGCGAGATGGGGTGTCTGCTCTCTGCGCTTCC 115  
Db 1 GTTGTCTGAAGGCGCGCGCGCGCGCGAGATGGGGTGTCTGCTCTCTGCGCTTCC 60  
Qy 116 GGATCTCTTGTCTGTGCTCTCAGCGTGGCCCGGCTGTGCAAGCAAGATGTCATCAGA 175  
Db 61 GGATCTCTTGTGTGTGCTCTCAGCGTGGCCCGGCTGTGCAAGCAAGATGTCATCAGA 120  
Qy 176 GCGTGGCCAGCGATGGGCCCAAGCAGACCCAGCTGCTTGGCAAMGGCCAGAGCCGTGG 235  
Db 121 GCGTGGCCAGCGATGGGCCCAAGCAGACCCAGCTGCTTGGCAAMGGCCAGAGCCGTGG 180  
Qy 236 CTCCCAAAACCGAGACCGCGCGCGCGCGAGTATGTGGGCCCAAGTGTGATACCTCCGCACT 295  
Db 181 CTCCCAAAACCGAGACCGCGCGCGCGAGTATGTGGGCCCAAGTGTGATACCTCCGCACT 240  
Qy 296 GGGCCCGCGGAGTTCTCTGTGGCCCATGACCTTGGCCTGGCTGTGCGCCGTGGAGA 355  
Db 241 GGGCCCGCGGAGTTCTCTGTGGCCCATGACCTTGGCCTGGCTGTGCGCCGTGGAGA 300  
Qy 356 TGATGACATGAGCAGACCCCGCTACGATGAGACCGCTTGGCGTGTCTTCCGCGCA 415  
Db 301 TGATGACATGAGCAGACCCCGCTACGATGAGACCGCTTGGCGTGTCTTCCGCGCA 360  
Qy 416 GCCCGCGCGCATGCCAGCTGATGCTGGGCCGCGACACTCAACCAAGATGGCCCGAG 475  
Db 361 GCCCGCGCGCATGCCAGCTGATGCTGGGCCGCGACACTCAACCAAGATGGCCCGAG 420  
Qy 476 CGCTTGCAGAGTCTACAGCAGATGTCGAGCCGCGCTACGATGCTCTCAATGGAGAGT 535  
Db 421 CGCTTGCAGAGTCTACAGCAGATGTCGAGCCGCGCTACGATGCTCTCAATGGAGAGT 480  
Qy 536 GCGCCACGAGAGAGGCTACTACATATTCCTACTGCTGTGTGAAGGGCTGTGCGACGCA 595  
Db 481 GCGCCACGAGAGAGGCTACTACATATTCCTACTGCTGTGTGAAGGGCTGTGCGACGCA 540  
Qy 596 TCGTGCCTGTGAGCATCTACATCCAGAGCTGCCCACTACAGGCCAGAGGCC 645  
Db 541 TCGTGCCTGTGAGCATCTACATCCAGAGTGAAGGGCCGAGCCGACCGGCC 590

## RESULT 4

US-10-104-047-262  
; Sequence 262, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 262  
; LENGTH: 3050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-262

Query Match 59.6%; Score 491; DB 17; Length 3050;  
Best Local Similarity 97.1%; Pred. No. 8.4e-127;  
Matches 500; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 131 GCTCCAGCGTGGCGCGCGCTGTGCAAGCAGAGGTGTCATCAGACGCTGGCCACCGATG 190  
Db 305 GCTCCAGCGTGGCGCGCGCTGTGCAAGCAGAGGTGTCATCAGACGCTGGCCACCGATG 364  
Qy 191 GCCCAAGCAGACCCAGCTTCCCTGCGCAAGGCCAGAGCCGTGCTCCAAACCCAGCA 250  
Db 365 GCCCAAGCAGACCCAGCTTCCCTGCGCAAGGCCAGAGCCGTGCTCCAAACCCAGCA 424  
Qy 251 GCCCGGGGAGTATGTGTGTCGCAAGCTGTGATGACTCTGTCAACTGGGCGCGGAGTT 310  
Db 425 GCCCGGGGAGTATGTGTGTCGCAAGCTGTGATGACTCTGTCAACTGGGCGCGGAGTT 484  
Qy 311 CTCTGTGGCCCATGACCTTCCGCTGGCTGTGCGCGCGCTGTGAGATGATGACATGGCAG 370  
Db 485 CTCTGTGGCCCATGACCTTCCGCTGGCTGTGCGCGCGCTGTGAGATGATGACATGGCAG 544  
Qy 371 CACCCCGCTACGACATGAGACCGCTTGGCGTGTCTTCCGCGCCAGCCCGCCAGTCCG 430  
Db 545 CACCCCGCTACGACATGAGACCGCTTGGCGTGTCTTCCGCGCCAGCCCGCCAGTCCG 604  
Qy 431 ACGTATGATGTGGCGCGGCAACCTCAACCAAGATGGCCCGCTTGGCAAGTCT 490  
Db 605 ACGTATGATGTGGCGCGGCAACCTCAACCAAGATGGCCCGCTTGGCAAGTCT 664  
Qy 491 ACGACAGATCCCGAGCCGCGCTTACGCTGTCTCCATGGGAGCTGCGCAAGGAGG 550  
Db 665 ACGACAGATCCCGAGCCGCGCTTACGCTGTCTCCATGGGAGCTGCGCAAGGAGG 724  
Qy 551 GCTACTACACTATTTCTTACTTGGTGTGTGAGGGGCTGCGACCGCATCTGCTCCGTGACA 610  
Db 725 GCTACTACACTATTTCTTACTTGGTGTGTGAGGGGCTGCGACCGCATCTGCTCCGTGACA 784  
Qy 611 TCTACATCCAGAGCTGCCCACTACGCGCCAGGCC 645  
Db 785 TCTACATCCAGAGTGAAGGGCCGAGCCGACCGGCC 819

## RESULT 5

US-10-104-047-914  
; Sequence 914, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:

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; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 914
; LENGTH: 3089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-914

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Query Match      51.8%; Score 427.2; DB 17; Length 3089;
Best Local Similarity 97.1%; Pred. No. 4,9e-109;
Matches 435; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 198 CAGCACCACCGCTCCCTGCTCCAAAGCCAGACCGCTGCTCCAAACCCAGACCGCGGG 257
DB 411 CAGCACCACCGCTCCCTGCTCCAAAGCCAGACCGCTGCTCCAAACCCAGACCGCGGG 470
QY 258 CGAGTATGTGTGGTGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
DB 471 CGAGTATGTGTGGTGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
QY 318 GCCCATGACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 377
DB 531 GCCCATGACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
QY 378 CTACGACATGAGACCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 437
DB 591 CTACGACATGAGACCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
QY 438 GATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 497
DB 651 GATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 710
QY 498 GATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 557
DB 711 GATGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 770
QY 558 CCACTATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 771 CCACTATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
QY 618 CCCAGGCTGCGCCACCTACGAGCCGAGGCC 645
DB 831 CCCAGGCTGCGCCGAGCCGAGCCGCC 858

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RESULT 6
US-09-759-143-32/c
; Sequence 32, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaloos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-32

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Query Match      46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3.4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCGCTGTGACGACGAGGTGTCATCAGACGCTGCGCCACGATGCGCCCAAGCAG 200
DB 739 GGGGAGTGTGNNAGANNAGNGTTCNTTAGAGNNGGGCCACCGGGGCCCAAGGG 680
QY 201 CACCCAGCTGCTGCTGCAAGGCGCAGAGCCGTGCTCCCAACCCAGACCGCGCGCA 260
DB 679 GGANCCANCTTGCCNNCCAAAGNNAGAGCGGTGTTCCCAACCCAGNANCCGGGGGA 620
QY 261 GTATGTGTGCTCAAGCTGATGACTCTG---CACTGAGCGCCCGGAGTTCTCTGTG 317
DB 619 GATTTGGGGGCCAAGGGGATGACTTTGTGAACTGGGNCCTCCCGAGNTTTTGGN 560
QY 318 G---CCCATGACCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
DB 559 GGGCCNCAAGAACTTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 373 CCCCCTACGACATGAGACCGCTTTGGCGTGG--TCTTCGCGCAGCCCGCGCAGTCCG 430
DB 499 CCCCNNAGACATGACNCCGTTTGGGANNNTTTTGGGCGCAGCCCGGACGACTG 440
QY 431 ACCTCATGATCGTGGCCGACACCTACCAACAGATGAGCCCGCTTGGCAAGTCT 490
DB 439 A-GTNATGATGTGGCNGNANNTAACCAAAAGAGGCCCGCAGN-TTTGCNAGGTTT 382
QY 491 AGACCAAGTCCGGAGCGCGCTACGTGCTCTCATGAGGAGCTGCGCCACGAGAG 550
DB 381 AAGACCAAGTCCGGAGCGCGGAGGAGGAGGTTTCANAGGGAG-TGNGCCACGAGGAG 323
QY 551 GCTACTACCTATTTCTCACTCGGTGTGAGGGCTGCGACCCGATGCTGCTGCGTGA 610
DB 322 GGTAAACCACTATTCTTAATNGTGTGAGGGAGTGCACCGCATTTGCTCCGTGAAA 263
QY 611 TCTACATCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670
DB 262 TTNAATCCCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY 671 AGAGAAATCAAGCGGAGCGAGGCTGCAATCTGTGATCCGACGATGAGCCCGCGCG 730
DB 202 AGAGAAATCAAGCGGAGCGAGGCTGCAATCTGTGATCCGACGATGAGGCGCGCG 143
QY 731 GCGCGCGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
DB 142 GCGCGCGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 83
QY 791 AATTAACCTGCTCGGGCAAAAAA 824
DB 82 AATTAACCTGCTCGGGCAAAAAA 49

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RESULT 7
US-09-780-669-32/c
; Sequence 32, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

```



APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kairos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stoik, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C24  
CURRENT APPLICATION NUMBER: US/09/780,669  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-780-669-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACGAGGTTCATCAGAGCGTGGCCACCCATGCGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTCTNTTAGANNNGCCCAACCGGGGCCGAAAGG 680  
201 CACCCAGCTGCGCTGCCAAAGCCGAGACCGTGGCTCCAAACCCAGCAGCCGGGGGA 260  
679 GGANCCANCTTGGCCNCCAAAGNNAAGAGCGTGGCTCCAAACCCAGNNAACGGGGGA 620  
261 GTATGTGTGCGCAAGCTGATGACTGT--CAACTGGGCGCGCGGAGTTCTCTGTG 317  
619 GGATTTGGGGGCGCAAGGGGATGACTTTGTGAAACTGGGACCCCGGAGNTTTTGN 560  
318 G---CCCATGACCTTGGCGCTGCGCGCGCGTGCAGATGATGACATGGCAGC-A 372  
559 GGGCCNCAAGAACTTTTGGGTGNCCTGNTGNGCCGGAGGTGATGANAATNGCAGCA 500  
373 CCCCGCTACGACATGACCGCTTTGGCGTG--TCTTCCGCGCAGCCCGCGCGAGTCCG 430  
499 CCCGNNNAAGACATGANCCTGTTTGGGNGNTTTTGGGGCCAGCCCGAGCGAGTCTG 440  
431 ACCTCATGATGTGGCGCGGACACTCACAACAAGATGGCCCGCTTGGCAAGTCT 490  
439 A-GTNAATGATTTGGCNGNANNTAACAAGAGGCGCCCAAGNG-TTTGCAAGGTTT 382  
491 ACAGACGATGCGGAGCGCGCTACGCTGCTCCATGGGAGCTGCGCAACGAGAGAG 550  
381 AAGACAGATGCGGAGCGCGGANAAGTGTTCANAGGGAAG-TGNCACCAAGGANG 323  
551 GCTACTACACTATTTCTACTCGGTGTGTAGAGGGCTGGACCGCATCTGCGCGTGA 610  
322 GGTAANACCACTATTTCTTAATNGGTGTGTAGAGGAGTGGACCGCATTTGTGCGCGGAAA 263  
611 TCTACATCCGAGCTGCCCACTACGCGCGGAGCGCTGCTCTAGGACATCTCTGACGCTGC 670  
262 TTNAATCCGAGGCTGCCACCAACGAGCGCGGAGCGCTGTTTTANAGACATCTCTGACGCTGC 203

671 AGAGAAATCAACGCGGAGCGAGGCTGCAGATCTGTGTAACGAGTAGGCGCGCGCC 730  
202 AGAGAAATCAACGCGGAGCGAGGCTGCANATTTGTGTAACGAGTAGGCGCGCGCC 143  
731 GCGCGCGCGGAGCGCTGTGCGCTGTCTGTCTCCCAAGCTGCTTGTCTCCGTGAGTTGTC 790  
142 GCGCGCGCGGAGCGCTGTGCGCTGTCTGTCTCCCAAGCTGCTTGTCTCCGTGAGTTGTC 83  
791 AATAACCTGCGCTGCGGCAAAAAA 824  
82 AATAACCTGCGCTGCGGCAAAAAA 49

RESULT 8  
US-09-030-606-32/C  
Sequence 32, Application US/09030606  
Patent No. US20020081580A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F

NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David U.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-030-606-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACGAGGTTCATCAGAGCGTGGCCACCCATGCGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTCTNTTAGANNNGCCCAACCGGGGCCGAAAGG 680  
201 CACCCAGCTGCGCTGCCAAAGCCGAGACCGTGGCTCCAAACCCAGCAGCCGGGGGA 260  
679 GGANCCANCTTGGCCNCCAAAGNNAAGAGCGTGGCTCCAAACCCAGNNAACGGGGGA 620  
261 GTATGTGTGCGCAAGCTGATGACTGT--CAACTGGGCGCGCGGAGTTCTCTGTG 317  
619 GGATTTGGGGGCGCAAGGGGATGACTTTGTGAAACTGGGACCCCGGAGNTTTTGN 560  
318 G---CCCATGACCTTGGCGCTGCGCGCGCGTGCAGATGATGACATGGCAGC-A 372  
559 GGGCCNCAAGAACTTTTGGGTGNCCTGNTGNGCCGGAGGTGATGANAATNGCAGCA 500

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QY 373 CCGCGTACGACATGAGACCGCTTTGGCGTG-TCCTCCGCGACGCGCGCAGTCCG 430
D 499 CCGCGNNAAAGACATGAGCCGGTTTGGGNGNNTTTTGGGGCCAGCCGNGCCAGTCTG 440
QY 431 ACCTCATGATCGTGGCCGCGACACTCAACCAAGATGCGCCAGCGCTTCCGAAGTCT 490
D 439 A-GTATGATGTTGGCGNGNANNTAAACCAAAAAGAGGCGCCAGNG-TTTGCAAGTTT 382
QY 491 ACAGCAGATGCGGAGCGCGCTACGTGTCTCATGAGGAGCTCGGCCAAGCGAGAG 550
D 381 AAGACGAGATGCGGAGCGCGANAGTGTTCANAGGAG-TGAGCCAAAGGNGNG 323
QY 551 GCTACTACACTATTCTTACTCGTGTGTGAGGGGCTGCGACCGCATGTGCGCGTGA 610
D 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGNGCGACCGCATGTGTGCGCGTGA 263
QY 611 TCTACATCCGAGCGTCCGACCTAGAGCGAGGCGCTGCTTACAGGCATCTTGCAGTGC 670
D 262 TTAAATCCAGAGGTGCGCCACCNANGCGAGGCGCTGTATTANAGCATCTGCACTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTACCGCAGTACGCGCGCGC 730
D 202 AGAGGAANATCAAGCGGAGCGGAGGCTGCANATTTGTACCGCAGTACGCGCGCGC 143
QY 731 GCGCGCGCGGAGCGTGTGCGCGTCTGTCTGCTCCAGCTGTGTGTCCGTGAGGTTGC 790
D 142 GCGCGCGCGGAGCGTGTGCGCGTCTGTCTGCTCCAGCTGTGTGTCCGTGAGGTTGC 83
QY 791 AATAAACCTGCGCTCGGCAAAAAA 824
D 82 AATAAACCTGCGCTCGGCAAAAAA 49
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## RESULT 9

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US-09-822-827-32/c
; Sequence 32, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-827-32
```

```
Query Match 46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3,4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
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```
QY 141 GGGCCCGGCTGTGACGACAGAGGTGTCCATCAGAGCGTGGCCAGCGATGCGCCAGCAG 200
D 739 GGGGAGATGTGNNNAGANGNGTTTCTTAGANNNGGCCACCGGGGGCCCGAAGG 680
QY 201 CACCCAGCTGCGCTGCAAGGCGAGCGGTGTCCCAAAACCAAGCAGCGCGGCGA 260
D 679 GGANCCANCTTGCNNCCAAAGNNAAGGCGTGGTTCCTCAAAACCAAGNNAAGCGGGGA 620
QY 261 GTATGTGTGGCGAAGCTGATGACTCTG---CAACTGGGCGCGCGGAGTTCTCTG 317
D 619 GGATTTGGGGCGCAAGGGGATGACTTTGTGAAACTGGGNGCCCGCGAGNTTTTGN 560
```

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QY 318 G-----CCATACCTTGGGCTGTGCGCTGTGCGCGGTGAGATGATGACATGCGACG-A 372
D 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGNTGNGCCCGGAGAGTATGTAANATNGCAACAA 500
QY 373 CCGCGCTACGACATGAGACCGCTTGGGGTGG--TCCTCCGCGCGACCGCGCGCAGTCCG 430
D 499 CCGCGNNAAAGACATGAGCCGGTTTGGGNGNNTTTTGGGGCCAGCCGNGCCAGTCTG 440
QY 431 ACCTCATGATGTTGGCGCGGCACTCAACCAAGATGCGCCAGCGCTTCCGAAGTCT 490
D 439 A-GTATGATGTTGGCGNGNANNTAAACCAAAAAGAGGCGCCAGNG-TTTGCAAGTTT 382
QY 491 ACAGCAGATGCGGAGCGCGCTACGTGTCTCATGAGGAGCTGCGCCAAAGAGAG 550
D 381 AAGACGAGATGCGGAGCGCGANAGTGTTCANAGGAG-TGAGCCAAAGGNGNG 323
QY 551 GCTACTACACTATTCTTACTCGTGTGTGAGGGGCTGCGACCGCATGTGCGCGTGA 610
D 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGNGCGACCGCATGTGTGCGCGTGA 263
QY 611 TCTACATCCGAGCGTCCGACCTTACGCGCGAGGCGCTGCTTACGCGCATCTGCACTGC 670
D 262 TTAAATCCAGAGGTGCGCCACCNANGCGAGGCGCTGTATTANAGCATCTGCACTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTGTAACCGCAGTACGCGCGCGC 730
D 202 AGAGGAANATCAAGCGGAGCGGAGGCTGCANATTTGTACCGCAGTACGCGCGCGC 143
QY 731 GCGCGCGCGGAGCGTGTGCGCGTCTGTCTGCTCCAGCTGTGTGTCCGTGAGGTTGC 790
D 142 GCGCGCGCGGAGCGTGTGCGCGTCTGTCTGCTCCAGCTGTGTGTCCGTGAGGTTGC 83
QY 791 AATAAACCTGCGCTCGGCAAAAAA 824
D 82 AATAAACCTGCGCTCGGCAAAAAA 49
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## RESULT 10

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US-09-115-453-32/c
; Sequence 32, Application US/09115453B
; Patent No. US2002090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-115-453-32
```

```
Query Match 46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3,4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
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```
QY 141 GGGCCCGGCTGTGACGACAGAGGTGTCCATCAGAGCGTGGCCAGCGATGCGCCAGCAG 200
D 739 GGGGAGATGTGNNNAGANGNGTTTCTTAGANNNGGCCACCGGGGGCCCGAAGG 680
QY 201 CACCCAGCTGCGCTGCAAGGCGAGCGGTGTCCCAAAACCAAGCAGCGCGGCGA 260
D 679 GGANCCANCTTGCNNCCAAAGNNAAGGCGTGGTTCCTCAAAACCAAGNNAAGCGGGGA 620
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QY 261 GTATGTGTGGCCCAAGCTGATGACTCTGT---CAACTGGGCGCGCCGAGTCTCTGTG 317  
DB 619 GGATTTGGGGGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNTTTTTGN 560  
QY 318 G----CCCATGACCTTGGGCTGTGCTGCGCCGTGGAGATGATGACATGGCAGC-A 372  
DB 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTGGGAGGTATGNAATNACAGAA 500  
QY 373 CCCCCTACGACATGAGACCGCTTTGGGCTGG--TCTTCGCGGCGAGCCCGGCGCAGTCCG 430  
DB 499 CCCCNNAAAGACATGAGNCGGTTTGGGNGNNTTTTGGGCGCAGCCCGGCGAGTCTG 440  
QY 431 ACCTCATGATGTGTGGCCGCGCACTCAACCAAGATGGCCCGACGCTTGGCAAGTCT 490  
DB 439 A-GTNAATGATTTGTGGCNGNANNTAACAAGAGGCGCCAGNG--TTTGCAAGGTTT 382  
QY 491 ACGACCAAGATGCGGAGCGCGCTACGTGTCTCATGTGGAGAGCTGCGCCAAAGAGAG 550  
DB 381 AAGACCAAGATGCGGAGCGCGAGAGGTGTTCCANGGGAG--TGNCCCAACGNGNG 323  
QY 551 GCTACTACCACTATTCTCTACTCGGTGTGAGGGGCTGCGACCGGATGCTGCGCGTGA 610  
DB 322 GGTAAACCACTATTCTCTAATNGGTGTGAGGGGNTGCGACCGCATTTGTGCGCGTGA 263  
QY 611 TCTACATCCAGGCTGCGCCCACTACGCGCGAGGCTGTCTACGCGCATCTGCAAGTGC 670  
DB 262 TTNAATATCCAGGGTGTCCACANAGGCGGAGGCTGTGTTTANGGCATCTGCAAGTGC 203  
QY 671 AGAGGAAGATTAACGGGAGCGGAGGCTGCAATCTGTATCCGCAAGTACGCGCGCC 730  
DB 202 AGAGGAANATCAACGGGAGCGGAGGCTGCANATTTGTGTACCGCAGCTAAGGCGCGCC 143  
QY 731 GCGCGCGCGGAGGCTGTGCGCGTCTGTCTCCGACCGCTGTGTCTCCGAGGTTGTC 790  
DB 142 GCGCGCGCGGAGGCTGTGCGGTCTGTCTCCGACCGCTGTGTGTCTCCGAGGTTGTC 83  
QY 791 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 824  
DB 82 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 49

RESULT 11  
US-09-232-880-32/c  
; Sequence 32, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jianshun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; FILE REFERENCE: 210121.428C6  
; CURRENT APPLICATION NUMBER: US/09/232, 880  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-232-880-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 34e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

QY 141 GGGCGCGGCTGTGACGACGACGAGTGTTCATCAAGCGCTGCGCAACCGATGCGCCCAAGCAG 200  
DB 739 GGGGGAATGTGNNNAGANAGNGTTTCTTATGAGANNGGCCCAACGGGGCGCGAAGGG 680

QY 201 CACCCAGCTGCGCTGCGCAAGCCGAGCCGTGGCTCCCAACCCAGCAGCCGCGCGCA 260  
DB 679 GGANCCANCTTGGCCNNCAAGANNAGAGCGCTGGGTTCCCAACCCAGNANCCGGGGGA 620  
QY 261 GTATGTGTGTGGCCCAAGCTGATGACTCTGT---CAACTGGGCGCGCCGAGTCTCTGTG 317  
DB 619 GGATTTGGGGGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNTTTTTGN 560  
QY 318 G----CCCATGACCTTGGGCTGTGCTGCGCCGTGGAGATGATGACATGGCAGC-A 372  
DB 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTGGGAGGTATGNAATNACAGAA 500  
QY 373 CCCCCTACGACATGAGACCGCTTTGGGCTGG--TCTTCGCGGCGAGCCCGGCGCAGTCCG 430  
DB 499 CCCCNNAAAGACATGAGNCGGTTTGGGNGNNTTTTGGGCGCAGCCCGGCGAGTCTG 440  
QY 431 ACCTCATGATGTGTGGCCGCGCACTCAACCAAGATGGCCCGACGCTTGGCAAGTCT 490  
DB 439 A-GTNAATGATTTGTGGCNGNANNTAACAAGAGGCGCCAGNG--TTTGCAAGGTTT 382  
QY 491 ACGACCAAGATGCGGAGCGCGCTACGTGTCTCATGTGGAGAGCTGCGCCAAAGAGAG 550  
DB 381 AAGACCAAGATGCGGAGCGCGAGAGGTGTTCCANGGGAG--TGNCCCAACGNGNG 323  
QY 551 GCTACTACCACTATTCTCTACTCGGTGTGAGGGGCTGCGACCGGATGCTGCGCGTGA 610  
DB 322 GGTAAACCACTATTCTCTAATNGGTGTGAGGGGNTGCGACCGCATTTGTGCGCGTGA 263  
QY 611 TCTACATCCAGGCTGCGCCCACTACGCGCGAGGCTGTCTACGCGCATCTGCAAGTGC 670  
DB 262 TTNAATATCCAGGGTGTCCACANAGGCGGAGGCTGTGTTTANGGCATCTGCAAGTGC 203  
QY 671 AGAGGAAGATTAACGGGAGCGGAGGCTGCAATCTGTATCCGCAAGTACGCGCGCC 730  
DB 202 AGAGGAANATCAACGGGAGCGGAGGCTGCANATTTGTGTACCGCAGGTAAAGGCGCGCC 143  
QY 731 GCGCGCGCGGAGGCTGTGCGCGTCTGTCTCCGACCGCTGTGTCTCCGAGGTTGTC 790  
DB 142 GCGCGCGCGGAGGCTGTGCGGTCTGTCTCCGACCGCTGTGTGTCTCCGAGGTTGTC 83  
QY 791 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 824  
DB 82 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 49

RESULT 12  
US-09-895-793-32/c  
; Sequence 32, Application US/09895793  
; Publication No. US20020192763A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jianshun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yudi  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Ketter, Marc W.  
; APPLICANT: Stoik, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Derrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Heppler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Baesols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-32
```

```

Query Match          46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3.4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
```

```

QY 141 GGGCCCGGCTGTGACGACGAGTGTCCATCAGACCGTGGCCACCGATGGCCCAAGCAG 200
DB 739 GGGGATGTTGNNNAGANGGTTTCTTGAAGNNGGCCACCGGGGCCGAGAGG 680
QY 201 CACCCAGCTGCTGCTGCCAAGGCGAAGCCGTGCTCCAAACCCAGACCGGGGCGA 260
DB 679 GGANCCANCTTGCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGGCCAGTGTGATGACCTGT---CAACTGGGCGCCCGGAGTTCTCTGTG 317
DB 619 GGATTTGGGGGCGAAGGGGATGACTTTGTGAACCTGGAGCCCGCCGAGNTTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCGCGTGGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGTTGNCCTGNTGNGCCCGGAGATGATGANAATNGCAGCA 500
QY 373 CCGGCTACGACATGAGACCGCTTTGGCGTG--TCTTCCGCGCAAGCCCGGCCAGTCCG 430
DB 499 CCGGNNNAGACATGAGCCGGTGGGAGNNTTTTTTGGGGCGCAGCCCGNCGCAGTCTG 440
QY 431 ACGTATGATGTGGCGCGGACACTCACCAACAAGATGGCCCGGCTTCGCAAGGTC 490
DB 439 A-GTATGATTTGTGGCNGNANNTAACCAAAAGAGGCCCGCAGNG-TTTGCAAGGTTT 382
QY 491 ACGACCATGATCCGAGCGCGCTACGTTCTTCATGGGAGCTGCGCAACGAGAGAG 550
DB 381 AAGACCAAGATGCCGAGCGCGANAGAGTGTTCANGGGAG-TGNGCCAAAGGNGNG 323
QY 551 GCTACTACCACTATTTCTACTCGGTGAGAGGGCTGCGACCGCATGTGCGCTGGACA 610
DB 322 GGTAAACCACTATTTCTTAATGAGTGTGAGGGGNTGCGACCGCATTTGTGCGGTGAAA 263
QY 611 TCTACATCCAGAGCTGCGCACTTACGCGGAGGCGCTGCTACAGGATCTTGAAGTGC 670
DB 262 TTNAATATCCAGGGGTGCCAANANNGGCCAGAGGCGCTTTTANAGGATCTTGAAGTGC 203
QY 671 AGAGAGATATCAAGCGGAGCGAGCGCTGCAATCTGTACCCGAGGTAGCGCGCGCC 730
DB 202 AGAGAGATATCAAGCGGAGCGAGCGCTGCANATTTGTACCGCAGGTAGGCGCGCGCC 143
QY 731 GCGCGCCGCGGAGCGCTGCGCGCTGCTGCCAGAGCTGTGTCCTCCGTAGGTTGTC 790
DB 142 GCGGCGCGCGGAGCGCTGTGCGCTGCTGCCAGGCTGATGTGTGTCGCGAGGTTGTC 83
QY 791 AATTAACCTGCTCTCGGCAAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCTCTGNNAAAAAAAAAAAAA 49
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RESULT 13
US-09-895-814-32/c
; Sequence 32; Application US/09895814
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; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiansun, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ketter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-32
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Query Match          46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3.4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
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QY 141 GGGCCCGGCTGTGACGACGAGTGTCCATCAGACCGTGGCCACCGATGGCCCAAGCAG 200
DB 739 GGGGATGTTGNNNAGANGGTTTCTTGAAGNNGGCCACCGGGGCCGAGAGG 680
QY 201 CACCCAGCTGCTGCTGCCAAGGCGAAGCCGTGCTCCAAACCCAGACCGGGGCGA 260
DB 679 GGANCCANCTTGCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGGCGCAAGCTGATGACCTGT---CAACTGGGCGCCCGGAGTTCTCTGTG 317
DB 619 GGATTTGGGGGCGAAGGGGATGACTTTGTGAACCTGGAGCCCGCCGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCGCGTGGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGTTGNCCTGNTGNGCCCGGAGATGATGANAATNGCAGCA 500
QY 551 GCGGCTACGACATGAGACCGCTTTGGCGTG--TCTTCCGCGCAAGCCCGCGCGAGTCCG 430
DB 499 CCGGNNNAGACATGAGCCGGTTTGGGAGNNTTTTTTGGGGCCAGCCCGNCGCAGTCTG 440
QY 431 ACGTATGATGTGGCGGCGACACTCACCAACAAGATGGCCCGGCTTGCAGAGTCT 490
DB 439 A-GTATGATTTGTGGCNGNANNTAACCAAAAGAGGCCCGCCAGNG-TTTGCAAGGTTT 382
QY 491 ACGACCATGATCCGAGCGCGCTACGTTGTCTCCATGGGAGCTGCGCAACGAGAGAG 550
DB 381 AAGACCAAGATGCCGAGCGCGGANAAGTGTTCANAGGGAG-TGNGCCAAAGGNGNG 323
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Qy 551 GCTACTACACTATTTCTACTCGGTGTGTGTGAGGGGCTGGACCGGATCTGTGCGCCGTGACACA 610
Dy 322 GGTAAACCACTATTCTCAATNGGTGGTGGAGGGGTGGAGCCGATTTGTGCCCGTGGAAA 263
Qy 611 TCTACATCCAGGCTGCTGCCACCTTACGGCCGAGCCCTGCTCTAGCGCATCTCTGCACTGC 670
Dy 262 TTNAAATCCCGGGGTGGCCACCCANNGCCGAGGCCCTGTTTANNGCATCTCTGCACTGC 203
Qy 671 AGAGAAAGATCAAGCGGAGGAGGAGGAGGCTGATCTGTACCGGAGTATGAGCGCGCGCC 730
Dy 202 AGAGAAANATCAAGCGGAGGAGGAGGCTGCANATTGTGTACCGAGTATGAGCGCGCGCC 143
Qy 731 GCCCGCCGCGGAGGCTGTGCGCGCTGTCTGTCCCAAGCTGTGTGTCTCCGTGAGGTTGTC 790
Dy 142 GCGCGCCGCGGAGGCTGTGTGCGCTGTCTGTCCCAAGCTGTGTGTCTCCGAGGTTGTC 83
Qy 791 AATAAACCCTGCTCGGCGCAAAAAA 824
Dy 82 AATAAACCCTGCTCGGCGCAAAAAA 49
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## RESULT 14

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US-10-012-896-32/c
; Sequence 32, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kaios, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yahir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Babsois, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 65, 68, 92, 103, 171, 195, 219, 238, 240, 260, 288, 301,
; LOCATION: 317, 324, 327, 336, 345, 358, 395, 417, 419, 421, 424, 436,
; LOCATION: 449, 468, 470, 483, 493, 494, 507, 510, 512, 528, 531, 536,
; LOCATION: 554, 560, 568, 579, 628, 631, 656, 657, 664, 665, 672
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 676, 703, 704, 711, 718, 721, 726, 727, 728, 741, 742, 744,
; LOCATION: 745, 749, 753, 757, 759, 773, 787
; OTHER INFORMATION: n = A,T,C or G
; US-10-012-896-32
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Query Match 46.7%; Score 384.6; DB 13; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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Qy 141 GGGCCCGGCTGTGACGAGCAGAGGTGTTCATCAAGCGCTGGCCACCGATGCGCAAGCAG 200
Dy 739 GGGGATGTGTNNNANAGANGNGTTCNTTAGAGNNNGGCCACCGGGGGCCGAAGG 680
Qy 201 CACCCAGCTGCTGCTGCAAGGCGCAGAGCCGTGCTCCCAAACCCAGCAGCGGGCGCA 260
Dy 679 GGANCCANCTTGCNNCCNCCAAAGNNAAGGCGGTGGTCCAAACCAGANAAACGGGGGA 620
Qy 261 GTATGTGTGCGCAAGCTGATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
Dy 619 GGATTTGGGGGCGCAAGGGGATGACTTGTGTGAAACTGGAGCCCGCGAGTTTTCGN 560
Qy 318 G----CCCATGACCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
Dy 559 GGGCGNCAAGAACTTTTGGTTGNCCTGTGTGNGCCCGGAGGTGATGNANATNGCAGCA 500
Qy 373 CCGCGCTACGACATGAGACCGCTTGGCGTGG--TCTTCCGGCCAGCCCGCCAGTCCG 430
Dy 499 CCGCGNNAAGACATGAGCCGCTTTTGGGNGNTTTTGGGGCCAGCCCGCCAGTCTG 440
Qy 431 ACGTCATGATGTGGCGCGGACACTCACCAACAAGATGGCCCGCTTGCAGAGTCT 490
Dy 439 A-GTNATGATTTGTGCGNGNANATTAACCAAAAGAGGCCCAAG--TTTGCAAGTTT 382
Qy 491 ACGACCAAGATGCGGAGCGCGCTACGTGTCTCCATGGGAGCTGCGCCAAAGAGAG 550
Dy 381 AAGACAGATCCCGAGCGCGGANAAGTGTTCANGGGAG--TNGCCAAAGGNGG 323
Qy 551 GCTACTACACTATTTCTACTCTGCTGTGTGAGGGGCTGCGACCGCATCTGCTCCGTGACA 610
Dy 322 GGTAAACCACTATTCTCAATNGGTGGTGGAGGGGTGGAACCGCATTTGTGCCGTGAAA 263
Qy 611 TCTACATCCAGGCTGCGCCACCTACGCGGAGGCGCTGCTCTAGCGGATCTCTGAGCTGC 670
Dy 262 TTNAAATCCAGGCTGCGCCACCCANNGCCGAGGCCCTGTTTANNGCATCTCTGAGCTGC 203
Qy 671 AGAGAAAGATCAAGCGGAGGAGGAGGCTGCAATCTGTGTACCGGAGTATGCGCGCGCC 730
Dy 202 AGAGAAANATCAAGCGGAGGAGGAGGCTGCANATTGTGTACCGGAGTATGCGCGCGCC 143
Qy 731 GCCCGCCGCGGAGGCTGTGCGCGCTGTCTGTCCCAAGCTGTGTGTCTCCGTGAGGTTGTC 790
Dy 142 GCGCGCCGCGGAGGCTGTGTGCGCTGTCTGTCCCAAGCTGTGTGTCTCCGAGGTTGTC 83
Qy 791 AATAAACCCTGCTCGGCGCAAAAAA 824
Dy 82 AATAAACCCTGCTCGGCGCAAAAAA 49
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## RESULT 15

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US-10-010-940-32/c
; Sequence 32, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaios, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Marc
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
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/ CURRENT APPLICATION NUMBER: US/10/010,940  
/ CURRENT FILING DATE: 2001-12-05  
/ NUMBER OF SEQ ID NOS: 575  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 32  
/ LENGTH: 789  
/ TYPE: DNA  
/ ORGANISM: Homo sapien  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (1)..(789)  
/ OTHER INFORMATION: n = A,T,C or G  
US-10-010-940-32

Query Match 46.7%; Score 384.6; DB 14; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
QY 141 GGGCCCGCTGTGCAGCAGCGTGTCCATCAGAGCGTGCACCGATGCGCCCAAGCAG 200  
Db 739 GGGGATGTGTNNAGANGNGTTCNTTAGAGNNGGCCACCGGGGCCCGCAAGG 680  
QY 201 CACCAGCGCTGCGCCCAAGGCGAGCGGTGCTCCAAACCCAGAGCGGGGCGA 260  
Db 679 GGANCCANTTGCCTCCAAAGANNAGAGCGGTGCTCCAAACCCAGNANCGGGGGA 620  
QY 261 GTATGTGTGCGCAAGCTGATGACCTGT--CAACTGAGCCCGCCGAGTTCCTGTG 317  
Db 619 GGATTTGGGGGCCAAGGGGATGACTTGTGAACCTGGNCCCGCGAGNTTTTGTGN 560  
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCTGCGCGTGAAGATGATGACATGGCAGC-A 372  
Db 559 GGGCNCAGAACTTTTGGTTGNCCTGNTGNCCTGGAGGTGATGNANATNGCAGCAA 500  
QY 373 CCCGCTACGACATGACCGCTTTGCGTGG--TCTTCGCGCCAGCGCGCCAGTCCG 430  
Db 499 CCCCNNAAAGACATGAGNCGGTTTGGGNGNTTTTGGGGCCAGCCCGNCCAGTCTG 440  
QY 431 ACGTCATGATGTGGCCCGGCACTACCAACAAGATGCCCCAGCGCTTGCAAGGTCT 490  
Db 439 A-GTNATGATTTGTGCGNNGNANNTAAACAAAGAGGCCCAAGNG-TTGCAAGGTTT 382  
QY 491 ACGACCAAGATGCGGAGCGGCTACGNTGTCTCATGGGAGAGCTGGCCCAACGAGAG 550  
Db 381 AAGACCAAGATGCGGAGCGGAGCGGAGGTTTCANGGGAG--TNGCCAAACGANGAG 323  
QY 551 GCTACTACACTATTCTACTCGTGTGTGAGGGGCTGCAACCGCATGTCGCGGTGACA 610  
Db 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGNTGGAACCGCATTTGTGCCGTGAAA 263  
QY 611 TCTACATCCCAAGGCTGCCCACTACGCGCGAGGCGCTGCTTACGCACTCTGCACTGC 670  
Db 262 TTNAAATCCCAAGGTTGCCCAACNANNGCCGAGGCCCTGTTTANNGCATCTGCACTGC 203  
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTAACCGAGGTAGGCGCGCGCC 730  
Db 202 AGAGGAANATCAAGCGGAGCGGAGGCTGCANATTTGTACCGCAGGTAGGCGCGCGCC 143  
QY 731 GCGGCGCGCGGAGCTGTGCGCGCTCTGTGCCCAAGCTGTGTCCTGCGTGAAGTTGTC 790  
Db 142 GCGGCGCGCGGAGCTGTGCGCGCTCTGTGCCCAAGCTGTGTCCTGCGTGAAGTTGTC 83  
QY 791 AATTAACCTGCGCGCGCAAAAAAAAAAAAAA 824  
Db 82 AATTAACCTGCGCGCGCAAAAAAAAAAAAAA 49

Search completed: March 22, 2005, 04:59:54  
Job time : 2947 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: March 21, 2005, 22:32:18 ; Search time 190 Seconds  
(without alignment)  
7096.274 Million cell updates/sec

Title: US-09-525-867-9  
Perfect score: 824  
Sequence: 1 cggctcgagcgctcgagcg.....cgggcaaaaaaaaaaaaaa 824

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 8181359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750.8	91.1	772	4	US-09-620-312D-670 Sequence 670, App
2	384.6	46.7	789	3	US-09-020-956-32 Sequence 32, Appl
3	384.6	46.7	789	3	US-09-030-607-32 Sequence 32, Appl
4	384.6	46.7	789	3	US-09-439-313-32 Sequence 32, Appl
5	384.6	46.7	789	3	US-09-352-616A-32 Sequence 32, Appl
6	384.6	46.7	789	3	US-09-232-149A-32 Sequence 32, Appl
7	384.6	46.7	789	4	US-09-159-812-32 Sequence 32, Appl
8	384.6	46.7	789	4	US-09-636-215-32 Sequence 32, Appl
9	384.6	46.7	789	4	US-09-685-166A-32 Sequence 32, Appl
10	384.6	46.7	789	4	US-09-115-453-32 Sequence 32, Appl
11	384.6	46.7	789	4	US-09-688-489-32 Sequence 32, Appl
12	384.6	46.7	789	4	US-09-679-426-32 Sequence 32, Appl
13	384.6	46.7	789	4	US-09-759-143-32 Sequence 32, Appl
14	384.6	46.7	789	4	US-09-651-236-32 Sequence 32, Appl
15	277.6	33.7	2378	4	US-09-270-767-14895 Sequence 14895, A
16	236.8	28.7	275	4	US-09-313-294A-6583 Sequence 6583, Ap
17	161.4	19.6	666	4	US-09-252-991A-15142 Sequence 15142, A
18	161.4	19.6	966	4	US-09-252-991A-14622 Sequence 14622, A
19	152	18.4	4403765	3	US-09-103-840A-2 Sequence 2, Appl
20	152	18.4	4411529	3	US-09-103-840A-1 Sequence 1, Appl
21	143.2	17.4	513	4	US-09-902-540-4615 Sequence 4615, Ap
22	143.2	17.4	27490	4	US-09-902-540-1227 Sequence 1227, Ap
23	127.2	15.4	690	4	US-09-489-039A-5374 Sequence 5374, Ap
24	119.6	14.5	615	4	US-09-248-796A-2829 Sequence 2829, Ap
25	112.2	13.6	58909	4	US-09-596-002-30 Sequence 30, Appl
26	110.2	13.4	708	4	US-09-540-236-467 Sequence 467, App
27	92.8	11.3	798	4	US-09-489-039A-2763 Sequence 2763, Ap

28	92	11.2	735	4	US-09-543-681A-43 Sequence 43, Appl
29	79	9.6	684	4	US-09-328-352-581 Sequence 581, App
30	79	9.6	640681	4	US-09-790-988-1 Sequence 1, Appl
31	52.4	6.4	2322	4	US-09-476-242-20 Sequence 20, Appl
32	52.4	6.4	2541	4	US-09-476-242-9 Sequence 9, Appl
33	52.4	6.4	2541	4	US-09-476-242-11 Sequence 11, Appl
34	50.8	6.2	2322	4	US-09-476-242-18 Sequence 18, Appl
35	50.8	6.2	2352	4	US-09-476-242-26 Sequence 26, Appl
36	50.8	6.2	2541	4	US-09-476-242-10 Sequence 10, Appl
37	49.2	6.0	2322	4	US-09-476-242-19 Sequence 19, Appl
38	49.2	6.0	2541	4	US-09-476-242-12 Sequence 12, Appl
39	47.8	5.8	891	4	US-09-252-991A-10527 Sequence 10527, A
40	47.8	5.8	1320	4	US-09-252-991A-10535 Sequence 10535, A
41	47.8	5.8	1473	4	US-09-252-991A-10639 Sequence 10639, A
42	47.8	5.8	3843	4	US-09-252-991A-1430 Sequence 1430, Ap
43	47.8	5.8	5337	4	US-09-252-991A-1588 Sequence 1588, Ap
44	47.4	5.8	1968	4	US-09-902-540-1231 Sequence 1231, Ap
45	47.4	5.8	17726	4	US-09-902-540-1148 Sequence 1148, Ap

## ALIGNMENTS

RESULT 1  
US-09-620-312D-670  
Sequence 670, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Ruihong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yundong

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radjic T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: PL FL\_genes Version 1.0

SEQ ID NO 670

LENGTH: 772

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (124)..(665)

US-09-620-312D-670

Query Match

Best Local Similarity 99.1%; Pred. No. 3.9e-165;

Matches 755; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 63 GAAGCGGAGCGCAAGATGGCGGTCTGAGCTCTGCGGCGGCTTCGAGATCCT 122  
DB 8 GAAGCGGAGCGCAAGATGGCGGTCTGAGCTCTGCGGCGGCTTCGAGATCCT 67

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QY 123 TGGTCTGCGCTCCAGCGTGGGCGCGCTGTGCGAGGACAGAGGTGTCATGAGACGTGGC 182
DB 68 TGGTCTGCGCTCCAGCGTGGGCGCGCTGTGCGAGGACAGAGGTGTCATGAGACGTGGC 127
QY 183 CACCGATGGCCCAACAGCAGCCAGACCTGGCCCTGCGAAAGGCCAGAGCCGTGGCTCCAA 242
DB 128 CACCGATGGCCCAACAGCAGCCAGACCTGGCCCTGCGAAAGGCCAGAGCCGTGGCTCCAA 167
QY 243 ACCGAGAGCCGGGGCGAGTATGTGTGGCCAGCGTGGATGACCTGCTCAACTGGGGCCG 302
DB 188 ACCGAGAGCCGGGGCGAGTATGTGTGGCCAGCGTGGATGACCTGCTCAACTGGGGCCG 247
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DB 248 CCGAGTCTCTGTGGGCCCATGACCTTGTGGCTGGCTGGCGCCGTGGAGATGATGCA 307
QY 363 CATGGAGCAGCCCGCTACGACATGAGACCGCTTGGGGGTGTCTTCCGGCCAGCCCGG 422
DB 308 CATGGAGCAGCCCGCTACGACATGAGACCGCTTGGGGGTGTCTTCCGGCCAGCCCGG 367
QY 423 CCAATCCGACGTCTGATTCGTGGCGGACACTCACCACAGATGGCCCGAGCGCTTG 482
DB 368 CCAATCCGACGTCTGATTCGTGGCGGACACTCACCACAGATGGCCCGAGCGCTTG 427
QY 483 CAAAGTCTACGACAGATGCGGAGCGGCTACGTGTCTCATGGGAGCTGGCCAA 542
DB 428 CAAAGTCTACGACAGATGCGGAGCGGCTACGTGTCTCATGGGAGCTGGCCAA 487
QY 543 CGAGAGAGGCTACTACCACTATTCTACTCGTGTGAGAGGGCTGGAGCCGATGGTGC 602
DB 488 CGAGAGAGGCTACTACCACTATTCTACTCGTGTGAGAGGGCTGGAGCCGATGGTGC 547
QY 603 CGTGAACATCTACCTCCAGGCGCTGACCTTACGCGGAGCCCTGCTTACGAGATCT 662
DB 548 CGTGAACATCTACCTCCAGGCGCTGACCTTACGCGGAGCCCTGCTTACGAGATCT 607
QY 663 GCGAGCTGCGAGAGATGATCAAGCGGAGCGAGGCTGAGATCTGTGACCGAGGTAGCG 722
DB 608 GCGAGCTGCGAGAGATGATCAAGCGGAGCGAGGCTGAGATCTGTGACCGAGGTAGCG 667
QY 723 CCGCGCGCGCGCGCGCGGAGGCTGTCCGCTGCTGTGCTCCAGCGCTGTGTGTCGGTG 782
DB 668 CCGCGCGCGCGCGCGCGGAGGCTGTCCGCTGCTGTGCTCCAGCGCTGTGTGTCGGTG 727
QY 783 AGGTGTCAATAAAGCTGCGCTCGGGCAAAAAAAAAAAAA 824
DB 728 AGGTGTCAATAAAGCTGCGCTCGGGCTCGGGCAAAAAAAAAAAAA 769

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## RESULT 2

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US-09-020-956-32/C
; Sequence 32, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillian, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998

```

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-020-956-32

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Query Match 46.7%; Score 384.6; DB 3; Length 789;
Best Local Similarity 75.9%; Pred. No. 4,2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCGCGCTGTGAGGACGAGGTGTCATGAGCGTGGGCCAGATGGCCCAAGCAG 200
DB 739 GGGGAGATGTGNNNAGGANGNTTTCTTGTAGAGNNAGGCCACCGGGGGCCCAAGG 680
QY 201 CACCCAGCTTCCTGCGCAAGGCGAGCCGTGGCTCCAAACCCAGCAGCGGGGCGA 260
DB 679 GAACCACTTGGCCNNCCAAAGNNAGGCGTGGGTTCCCAACCGAANCGGGGGA 620
QY 261 GTATGTGTGGCCCAAGCTGATGACCTGCT---CAACTGGGCGCCCGAGTTCTGTG 317
DB 619 GATTTGGGGGCCAAGGGGATGACTTGTGTAACCTGGANCCCCGAGATTTTTTGN 560
QY 318 G---CCATGACTTGGGCTGCGCTGTGCGCCGTGGAGATGATGACATGCGAGC-A 372
DB 559 GGGCCNCAAGAACTTTGGGTGNCCTGNTGNGCCGGGAGGTGATGANNNTGAGCAA 500
QY 373 CCCCCTGACGATGAGACCGCTTTGGCGTGG--TCTTCCGGGCCAGCCCGCGCATGCG 430
DB 499 CCCCNNMAGATGAGNCCGTTTTGGGANGTTTTTGGGGCCAGCCCGGCGCATGCTG 440
QY 431 AGTCAATGATCGTGGCGCGCACACTACCAACAGATGGCCCGACGCTTGCAAGGCT 490
DB 439 A-GTATGATGTGTGCGNGNANNTAACCAGAAAGAGGCCCGCAGNG-TTGGCAAGTTT 382
QY 491 ACGACAGATGCGGAGCGCGGCTACGTGTCTCATGGGAGCTGCGCAACGAGAGG 550
DB 381 AAGACCAATGCCGAGCGCGGANAAGTGTTCANAGGGAG-TGNGCAACGANGNG 323
QY 551 GCTACTACACTATTCTACTCGGTGTGAGGGGCTGCGACCGCATGTGCGCGTGACA 610
DB 322 GGTAAATACCACTATTCTAATNGTGTGAGGGGNTGCAACCGCATTTGTCCCGTGAAA 263
QY 611 TCTCATGCCAGGCTGCCCACTACGCGCGAGGCTGTCTTACCGGATCTTCAGCTGC 670
DB 262 TTAAATCTCCAGGGTGTCCACNANAGCCGAGGCCCTGTTTANGCATCTTCAGCTGC 203
QY 671 AGAGAAATCAAGCGGAGCGAGGCTGAGATCTGTACCGCAGATGACCGCGCGCC 730
DB 202 AGAGAAATCAAGCGGAGCGAGGCTGAGATCTGTACCGCAGATGACCGCGCGCC 143
QY 731 GCGCGCGCGGAGCGCTGTGCGCGCTCTGTGCTCCAGCGCTGTTGTGCTCCGTAGGTTGTC 790
DB 142 GCGCGCGCGGAGCGCTGTGCGCTGTGCTCCAGCGCTGTTGTGCTCCGTAGGTTGTC 83
QY 791 AATTAACCTGCTCGGGCAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCTCGGGCAAAAAAAAAAAAA 49

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## RESULT 3

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US-09-030-607-32/C
; Sequence 32, Application US/09030607

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Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030.607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-030-607-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;

Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACGAGGTTCATCAGAGCGTGCCACCGATGGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTNTTAAAGANNNGGCCACCGGGGCCGAAGG 680  
201 CACCCAGCTTCCCTGCAAGGCGCAGAGCGGTGCTCCAAACCCAGACCGGGGCGA 260  
679 GGANCCANCTTGCNNCCAAAGNNAGAGCGTGGGTTCCCAACCCAGNANCGGGGGA 620  
261 GTATGTGTGGCCAAAGCTGATGACTGTG---CACTGGGCGCGCGGAGTTCTGTG 317  
619 GGAATTTGGGGCCAAAGGGAGTGAATTTGTGAACTGGAGNCCCGCCGAGATTTTGN 560  
318 G----CCCATGACCTTCCGCTGCGCTGCTGCGCGCGTGAATGATGACATGGCAGC-A 372  
559 GGGGCGNCAAGAACTTTTGGTTGNCCTGNTGNGCCCGGAGGTATGANNATNGAGCAA 500  
373 CCCCCTAAGCATGAGACCGCTTTGGCGTGG--TCTTCGCGCCAGCCCGCGCATCGC 430  
499 CCCCNNNAAGACATGAGCCGGTTTGGGAGNATTTTGGGGCCGAGCCCGNCCAGTCTG 440  
431 AGCTCATGATGTGGCGGCGACATCACCACCAAGATGGCCCGCGGCTTGGCAAGTCT 490  
439 A-GTATATATTTGGCGNNGNANNTTAAACCAAAAGAGGCCCAANG--TTTGCAAGGTTT 382  
491 AGCAGCAGATGCGGAGCGCGCTACGTGTCTCCATGGGAGGCTGCCCAAGAGAGAG 550  
381 AAGACCAATGCGGAGCGCGANAAAGTGTTCANAGGGAG--TGNCCAAACGANGNG 323  
551 GCTACTACCACTATTTCTACTCGTGTGGAGGGGCTGGACCGCATGTCGCGCTGGACA 610  
322 GGTAAACCACTATTCCTAATGAGTGTGAGGGGAGTGGACCGCATGTGTGCGCGGAAA 263

US-09-439-313-32/C  
Sequence 32. Application US/09439313  
Patent No. 6229505

GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yugu  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark  
APPLICANT: Solk, John  
APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.427C9  
CURRENT APPLICATION NUMBER: US/09/439.313  
CURRENT FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 575  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32

LENGTH: 789

TYPE: DNA  
ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(789)

OTHER INFORMATION: n = A,T,C or G  
US-09-439-313-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;

Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACGAGGTTCATCAGAGCGTGCCACCGATGGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTNTTAAAGANNNGGCCACCGGGGCCGAAGG 680  
201 CACCCAGCTTCCCTGCAAGGCGCAGAGCGGTGCTCCAAACCCAGACCGGGGCGA 260  
679 GGANCCANCTTGCNNCCAAAGNNAGAGCGTGGGTTCCCAACCCAGNANCGGGGGA 620  
261 GTATGTGTGGCCAAAGCTGATGACTGTG---CACTGGGCGCGCGGAGTTCTGTG 317  
619 GGAATTTGGGGCCAAAGGGAGTGAATTTGTGAACTGGAGNCCCGCCGAGATTTTGN 560  
318 G----CCCATGACCTTCCGCTGCGCTGCTGCGCGCGTGAATGATGACATGGCAGC-A 372  
559 GGGGCGNCAAGAACTTTTGGTTGNCCTGNTGNGCCCGGAGGTATGANNATNGAGCAA 500  
373 CCCCCTAAGCATGAGACCGCTTTGGCGTGG--TCTTCGCGCCAGCCCGCGCATCGC 430

Db	499	CCCCGNNAAAGACATAGACCGCGTTTGGGGGNGNTTTTGGGGGCCACGCCGACAGTCTG	440
QY	431	ACGTCATGATCTGTCGGCCGCACTCAACPAACAAGTGGCCCCAGCGCTTGGCAAGTCT	490
Db	439	A-GTMAAGATTGTGGCGGNNANNTAAACCAAAAAGGGGCCCAAGN-TTGGCAAGTTT	382
QY	491	ACGACCGATGTCGGGAGCGCGCTAGTGTGTCCATGGGAGAGCTGTGGCCAAACGGAAGAG	550
Db	381	AAGACCGAGTGTGGCGAGCGCGGCAANAGTGTTCANGGGAGG-TGNCACCAACGNNGNG	323
QY	551	GCTACTACCACTATTCTCTGTGGTGTGAGGGGTGCGACCGCATCTGTGCCGTGGACA	610
Db	322	GGTAANACCACTATTCTTAATNGTGTGTGAGGGGWTGGACCGCATTTGTGCCCTGGAAA	263
QY	611	TCTACATCCCAAGGCTGCCCACTACGCGCGGAGGCCCTGCTCTACGCGATCTCTGACGTGC	670
Db	262	TTWAAATCCCAAGGCTGCCCAACNANNGCGAGAGCCCTCTTTTANNGCATCTGTGACGTGC	203
QY	671	AGAGGAAGATCAAGCGGGAGCGGAGCTCAGATCTGGTACCGGAGGTAAGCGCGCGCC	750
Db	202	AGAGGAANATCAAGCGGGAGCGGAGCTGCANATTGGTACCGGAGGTAAGGCGCGCGCC	143
QY	731	GCCGCGCGCGGAGCCTGTGCGCCGTCTGTCCCGACCTGCTTGTGCTCCGTGAAGTTGTC	790
Db	142	GCCGCGCGCGGAGCCTGTGCGCGTCTGTGCTCCCGACCTGNTGTGCCCGAGAGTTGTC	83
QY	791	AATTAACCTGCTCGCGGCAAAAAAAAAAAAAA	824
Db	82	AATTAACCTGCTCGCGGNNAAAAAAAAAAAAAA	49

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RESULT 5
US-09-352-616A-32/C
: Sequence 32, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OR INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.42768
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ. ID NOS: 472
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 789
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(789)
: OTHER INFORMATION: n = A,T,C or G
: US-09-352-616A-32

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	Query March Best Local Similarity Matches 521; Conservative	46.7%; 75.9%; 0;	Score 384.6; Pred. 4.2e-80; Mismatches 154; Indels 13; Gaps 7;	DB 3; Length 789;
QY	141 GGGCCCGCGCTGTGCAGACGAGAGTGTCCATCAGACGCGGCCACCGATGCGCCCAAGCAG			200
Db	739 GGGGAGATGTGTGNNMAGANGAGNTTTTCNTTGAAGANGGGCCACCGGGGGCCCGAAGG			680
QY	201 CACCCAGCTGCCTTCCCAAAGGCCAGAGCCGTGCTCCAAACCCAGACAGCGGGGCGCA			260
Db	679 GGANCCANCTTTGCGCANNCCAAAGNNAGAGCGCTGGTTCCAAACCCAGAAANCGGGGGGA			620
QY	261 GTATGTGTGTGGCCAAAGCTGATGACCTGCT---CAACTGGGGCGCCGGAGATTCTCTGTG			317
Db	619 GGAATTTGGGGGCCMAAGGGGATGACTTTTGTAAACTGGAGNCCCCCGAGAGNTTTTGTGN			560

QY 318 G-----CCCAATGACCTTCGGGCTTCGGGCTCGGCGCGGTGAGAGATGATGCAATATGGAGGC-A 3712  
 Db 559 GGGCCCAAGAACTTTGGGTGTGNCCTGATGAGCCGGGAGGTGATGATGANAATGCAAGCAA 5000  
 QY 373 CCCCCTCAAGACATGGAGCCGCTTTGGCGTG--TCTTCGCGCGCAAGCCCGGCGAGTCCG 4330  
 Db 499 CCCCAGNAAGACATGNCCTGGGTGTTGGGAGNGATTTTGTGGGCGCAAGCCGAGTCTG 4440  
 QY 431 ACGTCATGATCGGGCGCGGACACACTGACCAACAAGATGGGCCCGAGGCTTGGCAAGTCT 490  
 Db 439 A-GTATATGTTGTGGCGNGANANANTATCCAAAGAGGGGCCCCAGNG-TTGTGAAGGTTT 3820  
 QY 491 ACGACCAAGATGCGGAGCGCGGCGCTACGTGTCTCCAATGGAGAGCTGCGCCAAACGAGAG 550  
 Db 381 AAGACCGAGATGCGGAGCGCGGAGCCGANAAGTGTGTTCCANGGGGAG-TGNGCCAACGAGNG 323  
 QY 551 GGTACTACACATATTCTCTACTGGGTGGTGAAGGGGCTGGCAACGGCATCGTGGCCGTGGAACA 610  
 Db 322 GGTAANACCACTATTCTTATATGGGTGGTGAAGGGAGTGCACACGCATTTGGCCGTGGAAA 263  
 QY 611 TCTACATCCAGAGCTGCCCACTACGCGCGAGCGCTGCTCTTACGGCATCTCTGAGCTGC 670  
 Db 262 TTNAATCCACAGGGTGCCCAACNANAGCCGAGCGCTGTATTANGGCATCTCGAGCTGC 203  
 QY 671 AGAGAAAGATCAAGGGGAGCGGAGAGGTGCAATCTGTGATCCGCAAGTATGCGCCCGCGCC 730  
 Db 202 AAGAGAAANATCAAGGGGAGCGGAGAGGTGCAATTTGGTATCGCAGAGTATGAGGCCCGCGCC 143  
 QY 731 GCGCGCGCGGAGCTGTGCGCGTCTGTCCCACTGCTGTGTATCCGTAGAGTTGC 790  
 Db 142 GCGCGCGCGGAGCTGTGCGCGTCTGTCCCACTGNTTGTGTCCGAGAGTGTGC 83  
 QY 791 AATAAAGTCCCTCGGGCAAAAAAAAAAAAA 824  
 Db 82 AATAAAGTCCCTCGGGCAAAAAAAAAAAAA 49

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RESULT 6
; Sequence 32, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(785)
; OTHER INFORMATION: n = A,T,C or G
; US-09-232-149A-32

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Query Match	46.7%	Score 384.6	DB 3	Length 789
Best Local Similarity	75.9%	Pred. No. 4.2e-80		
Matches 527	Conservative	0	Mismatches 154	Indels 13
			Gaps	7
QY	141	GGGCCCGCGTGTCAAGSCACGAGTGTCATCAAGCGTGCCACCGATGGGCCCAAGAG	200	
Dp	739	GGGGGATGGTGGNNNAGANGNGTTTTCNTTAGAGNNGGCGCCACCGGGGCCCCGAAGCG	680	
QY	201	CACCCAGCTGCGCCCTGCGCAAGGCGCAGGCGTGTGCTCCCAAAACCGACAGCCGGGCGA	260	

Db 679 GANCCANCTTCCNNCCAAAGGCGTGGGTTCCCAACCAAGNANCGGGGGA 620  
Qy 261 GTATGTGTGGCCCAAGCTGATGACTCTGT---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGATTTGGGGCCAAAGGGGATGACTTTGTGAACTGGGNCCTCCCGAGNTTTTGTGN 560  
Qy 318 G---CCCATGACCTTGGGCTGGCTGTGCTGCGCGTGGAGATGATGACATGGCAG-A 372  
Db 559 GGGGNCNAAAGACTTTTGGGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 500  
Qy 373 CCGCGCTACGACATGAGACCGCTTTGGCGTG--TCTTCGCGCGACCGCGCGCACTCG 430  
Db 499 CCGCGNNAAGACATGAGNCCTGTTTGGGAGNTTTTGGGCGCAGCCGCGCACTGTG 440  
Qy 431 ACCTCATGATGTGGCGCGGACACTACCAAGATGGCCCGCAAGCTTGGCAAGTCT 490  
Db 439 A-GTATGATTTGTGGCGNANANATTAACCAAAAGAGGCGCCAGNG-TTGGCAAGGTTT 382  
Qy 491 ACACAGATGCGCGAGCGCGCTACGTCCTCCATGGGAGCTGCGCAAGGAGAG 550  
Db 381 AAGACAGATGCGCGAGCGCGAGAGAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323  
Qy 551 GCTACTACCACTATTCTACTCGGTGTGAGGGGCTGCGACCGCATGTGCTCGTGA 610  
Db 322 GGTAAACCACTATTCTTAATGAGTGTGAGGGGTCGACCGCATGTGCTCGTGA 263  
Qy 611 TCTACATCCAGGCTGCGGACCTACGCGCGAGGCGCTGTAGGCGCATCTGTGAGTGC 670  
Db 262 TTNAATCCAGGCTGCGGACCTACGCGCGAGGCGCTGTATTANAGCATCTGTGAGTGC 203  
Qy 671 AGAGAAAGATCAACCGGAGCGGAGCTGCAATCTGTAACGCAATGAGCGCGCGC 730  
Db 202 AGAGAAANATCAAGGGAGCGGAGCTGCANATTGTGTAACGCAATGAGCGCGCGC 143  
Qy 731 GCGCGCGCGGAGCTGTGCGCGCTGTCTGTCTCCAGCGCTGTGTCTCGTGAAGTTGC 790  
Db 142 GCGCGCGCGGAGCTGTGCGCGCTGTCTGTCTCCAGCGCTGTGTCTCGGAGGTTGC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAA 49

RESULT 7  
US-09-812-32/C  
; Sequence 32, Application US/09159812A  
; Patent No. 6613872  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
; FILE REFERENCE: 210121.428C5  
; CURRENT APPLICATION NUMBER: US/09/159,812A  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-159-812-32

Query Match 46.7%; Score 384.6; DB 4: Length 789;  
Best Local Similarity 75.9%; Pred. No. 4,2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCGGCTGTGACGACGAGGTGTCATCAGACGCTGGCCACGATGGCCCAAGCAG 200

141 GGGCGGCTGTGACGACGAGGTGTCATCAGACGCTGGCCACGATGGCCCAAGCAG 200

Db 739 GGGGATGTGTGNNAAGANGNTTTTONTTGAAGNNGGCCACCGGGGCGCGAAAGG 680  
Qy 201 CACCACCTGCGCTGCGCAAGGCGAGGCGTGGCTCCCAACCAAGCAGCGGGGGA 260  
Db 679 GANCCANCTTCCNNCCAAAGGCGTGGGTTCCCAACCAAGNANCGGGGGA 620  
Qy 261 GTATGTGTGGCCCAAGCTGATGACTCTGT---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGATTTGGGGCCAAAGGGGATGACTTTGTGAACTGGGNCCTCCCGAGNTTTTGTGN 560  
Qy 318 G---CCCATGACCTTGGGCTGGCTGTGCTGCGCGTGGAGATGATGACATGGCAG-A 372  
Db 559 GGGGNCNAAAGACTTTTGGGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 500  
Qy 373 CCGCGCTACGACATGAGACCGCTTTGGCGTG--TCTTCGCGCGACCGCGCGCACTCG 430  
Db 499 CCGCGNNAAGACATGAGNCCTGTTTGGGAGNTTTTGGGCGCAGCCGCGCACTGTG 440  
Qy 431 ACCTCATGATGTGGCGCGGACACTACCAAGATGGCCCGCAAGCTTGGCAAGTCT 490  
Db 439 A-GTATGATTTGTGGCGNANANATTAACCAAAAGAGGCGCCAGNG-TTGGCAAGGTTT 382  
Qy 491 ACACAGATGCGCGAGCGCGCTACGTCCTCCATGGGAGCTGCGCGCAAGGAGAG 550  
Db 381 AAGACAGATGCGCGAGCGCGAGAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323  
Qy 551 GCTACTACCACTATTCTACTCGGTGTGAGGGGCTGCGACCGCATGTGCTCGTGA 610  
Db 322 GGTAAACCACTATTCTTAATGAGTGTGAGGGGTCGACCGCATGTGCTCGTGA 263  
Qy 611 TCTACATCCAGGCTGCGGACCTACGCGCGAGGCGCTGTAGGCGCATCTGTGAGTGC 670  
Db 262 TTNAATCCAGGCTGCGGACCTACGCGCGAGGCGCTGTATTANAGCATCTGTGAGTGC 203  
Qy 671 AGAGAAAGATCAACCGGAGCGGAGCTGCAATCTGTAACGCAATGAGCGCGCGC 730  
Db 202 AGAGAAANATCAAGGGAGCGGAGCTGCANATTGTGTAACGCAATGAGCGCGCGC 143  
Qy 731 GCGCGCGCGGAGCTGTGCGCGCTGTCTGTCTCCAGCGCTGTGTCTCGTGAAGTTGC 790  
Db 142 GCGCGCGCGGAGCTGTGCGCGCTGTCTGTCTCCAGCGCTGTGTCTCGGAGGTTGC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAA 49

RESULT 8  
US-09-636-215-32/C  
; Sequence 32, Application US/09636215  
; Patent No. 6620822  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215

US-09-636-215-32/C  
; Sequence 32, Application US/09636215  
; Patent No. 6620822  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215

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; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-32

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Query Match      46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCCGCTGTGCAGCAGCGAGGTGCATCAGAGCGTGCACCGATGCGCCCAAGCAG 200
DB 739 GGGGGATGATGNNAGANGNGTTCNTTAGANNNGGCGCCACCGGGGCGCCGAAGG 680
QY 201 CACCCAGCCTGCTGCCCAAGCCAGCCGTGGCTCCCAACCAGACCGCGGGGGA 260
DB 679 GGANCCANCTTGCCNNCCAAAGNNAGAGCGGTGGTCCCAACCAGNANCGGGGGA 620
QY 261 GTATGTGTGCGCAAGCTGATGACCTGTG--CAACTGGGCGCGCCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCAAGGGGGATGACTTTGTGAACCTGGAGCCCGGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGCGCCCTGCGCTGCGCGCTGCGCGTGAATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGTTGNCCTGNTGNGCCGGAGAGTGAATGANAATNGCAGAA 500
QY 373 CCGCGCTACGACATGACCGCTTTGGCGTGG--TCTTCGCGCCAGCCCGCGCCAGTCCG 430
DB 499 CCGCGNNAAGACATGANCCTGGTTTGGGGNNTTTTTGGGGCCAGCCCGCCAGTCTG 440
QY 431 ACGTCATGATGCTGGCGCGCACTACCAACAAGATGGCCCCAGCGCTTGCAAGGTCT 490
DB 439 A-GTATGATGTTGGCNGNANNTAACAAGAGGGGCCCAAGG--TTTGCAAGGTTT 382
QY 491 ACGACAGATGCGGAGCGCGCTACCGTGTCTCATGGGGAGTGGGCCCAACGAGAGAG 550
DB 381 AAGACAGATGCGGAGCGCGCAAGAGTGTTCANNGGGAG--TNGCCCAACGAGNGAG 323
QY 551 GCTACTACACTATTTCTACTCGGTGTGAGGGGCTGCAACCGCATGTCGCGCTGACA 610
DB 322 GGTANACCACTATTTCTAATNGTGTGAGGGGNTGCAACCGCATTTGTGCGCTGAAA 263
QY 611 TCTCATCCCAAGGCTGCGCACTACCGCCAGGCGCTGCTCTACGCGATCTTGACGTTGC 670
DB 262 TTNAATTCGAGGTGCGCACCNANNGGCCAGAGCGCTGTTTANGGGATCTTGACGTTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGAGGCTGAGATCTGTACCGGAGGTAGCGCGCGCC 730
DB 202 AGAGGAANATCAAGCGGAGCGAGGCTGACANATTGTGTAACCGAGTAAAGGCGCGCC 143
QY 731 GCGCGCCCGGAGCGCTGCGCGCTGCTGTGCTCCAGCGCTGCTTGTGTCGCGTGAAGTTGTC 790
DB 142 GCGCGCCCGGAGCGCTGCGCGCTGCTGTGCTCCAGCGCTGTTGTGTCGCGNAGAGTTGTC 83
QY 791 AATTAACCTGCGCTCGGCAAAAAA 824
DB 82 AATTAACCTGCGCTCGGCAAAAAA 49

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RESULT 9
US-09-685-166A-32/c
; Sequence 32, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.

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; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-32

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Query Match      46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCCGCTGTGCAGCAGAGGTGTCATCAGAGCGTGCACCGATGCGCCCAAGCAG 200
DB 739 GGGGGATGATGNNAGANGNGTTCNTTAGANNNGGCGCCACCGGGGCGCCGAAGG 680
QY 201 CACCCAGCCTGCTGCCCAAGCCAGCCGTGGCTCCCAACCAGACCGCGGGGGA 260
DB 679 GGANCCANCTTGCCNNCCAAAGNNAGAGCGGTGGTCCCAACCAGNANCGGGGGA 620
QY 261 GTATGTGTGCGCAAGCTGATGACCTGTG--CAACTGGGCGCGCCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCAAGGGGGATGACTTTGTGAACCTGGAGCCCGGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGCGCCCTGCGCTGCGCGTGAATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGTTGNCCTGNTGNGCCGGAGAGTGAATGANAATNGCAGAA 500
QY 551 GCTACTACACTATTTCTACTCGGTGTGAGGGGCTGCAACCGCATGTCGCGCTGACA 610
DB 262 TTNAATTCGAGGTGCGCACCNANNGGCCAGAGCGCTGTTTANGGGATCTTGACGTTGC 203
QY 611 TCTCATCCCAAGGCTGCGCACTACCGCCAGGCGCTGCTCTACGCGATCTTGACGTTGC 670
DB 262 TTNAATTCGAGGTGCGCACCNANNGGCCAGAGCGCTGTTTANGGATCTTGACGTTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGAGGCTGACATCTGTGTACCGAGGTAGCGCGCGCC 730

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Db 202 AGAGGAANATCAACGGGAGCGAGGCTGCANATTGGTACCGAGGTAGGGCCGCC 143  
Qy 731 GCGCGCCCGGAGGCTGCGCGCTCTGTCCCGAGCCGCTGTGTCCCGTAGGTTGTC 790  
Db 142 GCGCGCCCGGAGGCTGTGCGCTGTCTCCCGAGCCGCTGTGTGTCCCGAGGTTGTC 83  
Qy 791 AATTAACCTGCGCTCGGCGCAAAAAAAAAA 824  
Db 82 AATTAACCTGCGCTCGGCGCAAAAAAAAAA 49

RESULT 10  
US-09-115-453-32/c  
; Sequence 32, Application US/09115453B  
; Patent No. 6657056  
; GENERAL INFORMATION:  
; APPLICANT: Xu, JIANGCHUN  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115.453B  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) ... (789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCGCGGCTGTGCAAGCAGAGGTTCATCAAGCTGTGCCACCGATGCCCAAGCAG 200  
Db 739 GGGGATGTGTGNNNAGANGGTTTTCNTTGAAGNNGGGCCACCGGCGCGAAGGG 680  
Qy 201 CACCCAGCTGCGCTGCAAAAGCGCAGCGGTCTCCCAACCCAGCAGCGGGGCGA 260  
Db 679 GGANCCANCTTGCCNNCCAAAGNNAAGGCGTGGGTTCCCAACCCAGNNAACGGGGGA 620  
Qy 261 GTATGTGTGCGCAAGCTGTGATGACTCTGT---CAACTGGGCGCGCGAGTTCTGTG 317  
Db 619 GGATTTGGGGCGCAAGGGGATGACTTTGTGAAACTGGGNCCTCCCGAGNTTTTTGN 560  
Qy 318 G----CCCATGACCTTGGGCTGTGCTGCGCGCGGTGAGATGATGCAATGGCAGC-A 372  
Db 559 GGGGCGNCAAGAACTTTGGGTTGNCCTGNTGNGCCCGGAGGTATGNAATNACAGCAA 500  
Qy 373 CCGCGCTACGACATGAGACCGCTTTGGCGTGG--TCTTCCGGCGCAGCCCGGCGCAGTCCG 430  
Db 499 CCGCGNNAAGACATGAGNCCGGTTTGGGNGNTTTTTTTGGGGCCAGCCCGAGCCAGTCTG 440  
Qy 431 ACCTCATGATCGTGGCGCGGCACTCACTCAACAAGATGGCCCGAGCGCTTGGCAAGTCT 490  
Db 439 A-GTNATGATGTGTGCGNGNANNTAACAAGAGAGGCGCCAGNG--TTTGCAAGGTTT 382  
Qy 491 ACGACCAAGATGCCGAGCGCGCTACGTTGCTCCATGGGAGCTGCGCAACGAGAG 550  
Db 381 AAGACCAAGATGCCGAGCGCGAGCAAGAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323  
Qy 551 GCTACTACCACTATTTCTACTCGGTGAGGAGGGGTGAGACCGATCGTGGCCGAGCA 610  
Db 322 GGTAAACCACTATTTCTTAATNGGTGTGAGGGGTGAGACCGCATTTGTGCGCGGAAA 263  
Qy 611 TCTACATCCAGGCTGCCCACTACGAGCGAGCGCTGCTCAAGGCACTCTGACGTGC 670

Db 262 TTNAATCCAGGGGTGCCACACNANGGCCAGGCGCTGTTTANAGCATCTTGACAGCTGC 203  
Qy 671 AGAGGAAGATCAAGCGGAGCGGAGCTGCAGATCTGTATCCGAGATAGCGCGCGCC 730  
Db 202 AGAGGAANATCAACGGGAGCGAGGCTGCANATTGGTACCGAGGTAGGGCCGCC 143  
Qy 731 GCGCGCCCGGAGGCTGCGCGCTCTGTCCCGAGCCGCTGTGTGTCCTCGGAGGTTGTC 790  
Db 142 GCGCGCCCGGAGGCTGTGCGCTGTCTCCCGAGCCGCTGTGTGTCCCGAGGTTGTC 83  
Qy 791 AATTAACCTGCGCTCGGCGCAAAAAAAAAA 824  
Db 82 AATTAACCTGCGCTCGGCGCAAAAAAAAAA 49

RESULT 11  
US-09-688-489-32/c  
; Sequence 32, Application US/09688489  
; Patent No. 6664377  
; GENERAL INFORMATION:  
; APPLICANT: Xu, JIANGCHUN  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427D2  
; CURRENT APPLICATION NUMBER: US/09/688.489  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) ... (789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-688-489-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCGCGGCTGTGCAAGCAGAGGTTCATCAAGCTGTGCCACCGATGCCCAAGCAG 200  
Db 739 GGGGATGTGTGNNNAGANGGTTTTCNTTGAAGNNGGGCCACCGGCGCGAAGGG 680  
Qy 201 CACCCAGCTGCGCTGCAAAAGCGCAGCGGTCTCCCAACCCAGCAGCGGGGCGA 260  
Db 679 GGANCCANCTTGCCNNCCAAAGNNAAGGCGTGGGTTCCCAACCCAGNNAACGGGGGA 620  
Qy 261 GTATGTGTGCGCAAGCTGTGATGACTCTGT---CAACTGGGCGCGCGAGTTCTGTG 317  
Db 619 GGATTTGGGGCGCAAGGGGATGACTTTGTGAAACTGGGNCCTCCCGAGNTTTTTGN 560  
Qy 318 G----CCCATGACCTTGGGCTGTGCTGCGCGCGGTGAGATGATGCAATGGCAGC-A 372  
Db 559 GGGGCGNCAAGAACTTTGGGTTGNCCTGNTGNGCCCGGAGGTATGNAATNACAGCAA 500  
Qy 373 CCGCGCTACGACATGAGACCGCTTTGGCGTGG--TCTTCCGGCGCAGCCCGGCGCAGTCCG 430  
Db 499 CCGCGNNAAGACATGAGNCCGGTTTGGGNGNTTTTTTTGGGGCCAGCCCGAGCCAGTCTG 440  
Qy 431 ACCTCATGATCGTGGCGCGGCACTCACTCAACAAGATGGCCCGAGCGCTTGGCAAGTCT 490  
Db 439 A-GTNATGATGTGTGCGNGNANNTAACAAGAGAGGCGCCAGNG--TTTGCAAGGTTT 382  
Qy 491 ACGACCAAGATGCCGAGCGCGCTACGTTGCTCCATGGGAGAGCTGCGCAACGAGAG 550  
Db 381 AAGACCAAGATGCCGAGCGCGAGCAAGAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323

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QY 551 GCTACTACCACTATCTCTACTCGTGTGATGAGGGCTGCGACCGCATCGTGGCCGTGGACA 610
DB 322 GGTAAACCACTATTCTTAATGATGTGAGGGGATGCCACCGCATTTGTGCGCGTGGAAA 263
QY 611 TCTACATCCGAGGCTGCTCCCACTACGCGCGAGCCCTGCTCTACCGGCATCTCCAGACTGC 670
DB 262 TTNAATATCCAGAGGTGCCACCNANAGCCGAGGCCCTGTTTANAGCATCTCGCACTGC 203
QY 671 AGAGGAAGATCAAGCCGAGCGGAGGAGCTGCAGATCTGTACCGCAGATAGCGCGCGCC 730
DB 202 AGAGGAATATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGAGGTAGGCGCGCGCC 143
QY 731 GCCCGCCGAGAGCTGTGCGCGCTGCTGTCCCAAGCTCTGTGTGCTCCGTAGGTTGTC 790
DB 142 GCCCGCCGAGAGCTGTGCGCGCTGCTGTCCCAAGCTCTGTGTGCTCCGTAGGTTGTC 83
QY 791 AATTAACCTGCTCGCGGCAAAAAA 824
DB 82 AATTAACCTGCTCGCGGCAAAAAA 49
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RESULT 12  
US-09-426-32/C  
Sequence 32, Application US/09679426

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Patent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)---(789)
OTHER INFORMATION: n = A,T,C or G
US-09-679-426-32
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Query Match 46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
QY 141 GGGCCGGCTGTGTCAGAGGTGTCATCAGAGGTGCGCCAGCGATGCGCCAAAGCAG 200
DB 739 GGGGAGATGTGNNNAGANGANGTTTCTTAAAGNNGGCCACCGGGGGCCGAAAGG 680
QY 201 CACCCAGCTGCTGCTGCAAGGCGAGGCGTGGCTCCCAAACCGACAGCGCGGGCGA 260
DB 679 GGANCACTTGCCNNCCAAAGNNAAGAGCGTGCGTTCCAAACCGAGNANAGGGGGGA 620
QY 261 GTATGTGTGGCCAGCTGATGACTCTGT---CACTGGGCGCGCGAGTTCTCTGTG 317
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DB 619 GGATTTGGGGGCCAAGGGGGATGACTTTGTGAATACTGGNCCCGCGGAGNTTTTGTG 560
QY 318 G-----CCATGACTTTGGCGCTGCGCTGCTGCGCGCGGAGATGATGATGACAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGGTTGATCTGNTGNGGCCGAGAGTGATGANAATNGCAGCAA 500
QY 373 CCGCGCTACGATGAGACCGCTTGGCGTG-TCCTCCGCGCAGCCCGCGCATGCG 430
DB 499 CCGGNNAGACATGACGCCGTTTGGGAGNTTTTGGGGCCAGCCCGGCGCATGCTG 440
QY 431 ACGTCATGATGCTGCGCGGCACTACACCAAGATGCCCCCGAGCGCTTGCAGAGTCT 490
DB 439 A-GTATGATTTGTGCMGNNANNTAACAAGAGAGGCCCAAG-TTTGCAAGGTTT 382
QY 491 ACGACAGATGCGGAGCGGCTACGTGCTCTCATATGAGGAGTGTGCGCAAGAGAG 550
DB 381 AAGACCAATGCGGAGCGCGGAGGAGGATTTCCAGCGGAG-TGNCACACGANGNG 323
QY 551 GCTACTACCACTATCTCTACTCGTGTGATGAGGGCTGCGACCGCATGTGCGCGTGGACA 610
DB 322 GGTAAACCACTATTCTTAATGATGTGAGGGGATGCCACCGCATTTGTGCGCGTGGAAA 263
QY 611 TCTACATCCGAGGCTGCTCCCACTACGCGCGAGCCCTGCTCTACCGGCATCTCGAGCTGC 670
DB 262 TTNAATATCCAGAGGTGCCACCNANAGCCGAGGCCCTGTTTANAGCATCTCGCACTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTATCCGACGTAGCGCGCGCC 730
DB 202 AGAGGAATATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGACGTAGGCGCGCGCC 143
QY 731 GCCCGCCGAGAGCTGTGCGCGCTGCTGTCCCAAGCTCTGTGTGCTCCGTAGGTTGTC 790
DB 142 GCCCGCCGAGAGCTGTGCGCGCTGCTGTCCCAAGCTCTGTGTGCTCCGTAGGTTGTC 83
QY 791 AATTAACCTGCTCGCGCAAAAAA 824
DB 82 AATTAACCTGCTCGCGCAAAAAA 49
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RESULT 13

US-09-759-143-32/C

Sequence 32, Application US/09759143

Patent No. 6800746

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolck, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Derrick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 789

TYPE: DNA

ORGANISM: Homo sapien

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(789)
OTHER INFORMATION: n = A,T,C or G
US-09-759-143-32
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Query Match 46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
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QY 141 GGGCCCCGCTGTGACGACGAGGTGTCATCAGAGGTGCGCCACCGATGCGCCCAAGCAG 200
DB 739 GGGGGATGTGTGNNNAGANGNTTTTNTTAGANNNGGCCACCGGGGGCCCGAAGGG 680
QY 201 CACCCAGCTGCGCTGCGCAAGGCGGAGCGGTGCTCCCAACCCAGCGCGGGCGA 260
DB 679 GGANCCANCTTGCCNNCCAAAGNAGAGCGGTGGTTCCCAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGGCCAGCTGTGATGACTCGT---CAACTGGGCGCGCGAGTTCTCTGTG 317
DB 619 GGATTTGGGGGCCAAAGGGGATGACTTTGTGAACAGGGGCCCGCGAGNTTTTGTGN 560
QY 318 G----CCCATGACCTTGCGCTGCGCTGTGCGCGCTGGAGATGATGACATGCGAGC-A 372
DB 559 GGGCCNCAGAACTTTGGGTGTCGNTGNGCCCGGAGGTGATGANAATNGCAGCAA 500
QY 373 CCGCGCTACGACATGACCGGTTTGGGCTGG--TCTTCCGCGCAGGCGCGCGAGTCCG 430
DB 499 CCGCGNNAAGCATGAGNCGGTTTGGGNGNTTTTGGGGCCAGCGCGCGCAAGTCTG 440
QY 431 ACCTGATGATCGTGGCGCGCACACTCAACAAGATGCGCCCGCTTGCAGAGTCT 490
DB 439 A-GTNATGATGTGTGCGNANANTTAACAAAAGAGGGCCCAAGNG--TTTGCAAGTTT 382
QY 491 ACGACCATGATGCGGAGCGCGCTACGTGTCTTCATGGGAGCTCGCGCAACGAGAG 550
DB 381 AAGCCAGATGCGCGAGCGCGGANAAGTGTTCANAGGGAG--TGNGCCAAACGNGNG 323
QY 551 GCTACTACACTATTCTACTCGGTGTGAGGGGCTGGACCGGATGTGCGCTGAGCA 610
DB 322 GGTAAACCACTATTCTTAATNGGTGTGAGGGGNTGAGACCGCATGTGTGCGTGA 263
QY 611 TCTACATCCAGAGCTGCGCACTTACGCGCGAGCGCTGCTCTACGGGATCTGTGAGCTGC 670
DB 262 TTNAATATCCAGAGGTGCGCACANAGCGAGCGCGCTGTTTANAGCATCTGTGAGCTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGCTGACATCTGTGATCCGAGGTAGCGCGCGCC 730
DB 202 AGAGGAANATCAAGCGGAGCGGAGCTGACANATTTGTACCGCAGGTAGGGCGCGCC 143
QY 731 GCGCGCGCGGAGCTGTGCGCGCTGTCTCCCGAGCGCTGTGTGTCTCCGTGAGGTGTC 790
DB 142 GCGCGCGCGGAGCTGTGCGCGCTGTCTCTCCCGAGCGCTGTGTGTCTCCGAGAGGTGTC 83
QY 791 AATTAACCTGCGCTCGGCAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCGCTCGGCAAAAAAAAAAAAA 49
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RESULT 14
US-09-651-236-32/c
Sequence 32, Application US/09651236
Patent No. 6818751
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GENERAL INFORMATION:

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APPLICANT: Xu, Jiaqun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuhui
APPLICANT: Henderson, Robert A.
APPLICANT: Kaios, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
```

```
APPLICANT: Scolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT FILING DATE: US/09/651.236
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(789)
OTHER INFORMATION: n = A,T,C or G
US-09-651-236-32
```

```
Query Match 46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;
```

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QY 141 GGGCCCCGCTGTGACGACGAGGTGTCATCAGAGGTGCGCCACCGATGCGCCCAAGCAG 200
DB 739 GGGGGATGTGTGNNNAGANGNTTTTNTTAGANNNGGCCACCGGGGGCCCGAAGGG 680
QY 201 CACCCAGCTGCGCTGCGCAAGGCGGAGCGGTGCTCCCAACCCAGCGCGGGCGA 260
DB 679 GGANCCANCTTGCCNNCCAAAGNAGAGCGGTGGTTCCCAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGGCCAGCTGTGATGACTCGT---CAACTGGGCGCGCGAGTTCTCTGTG 317
DB 619 GGATTTGGGGGCCAAAGGGGATGACTTTGTGAACAGGGGCCCGCGAGNTTTTGTGN 560
QY 611 TCTACATCCAGAGCTGCGCACTTACGCGCGAGCGCTGCTCTACGGGATCTGTGAGCTGC 670
DB 439 A-GTNATGATGTGTGCGNANANTTAACAAAAGAGGGCCCAAGNG--TTTGCAAGTTT 382
QY 671 AGAGGAAGATCAAGCGGAGCGGAGCTGACATCTGTGATCCGAGGTAGCGCGCGCC 730
DB 202 AGAGGAANATCAAGCGGAGCGGAGCTGACANATTTGTACCGCAGGTAGGGCGCGCC 143
QY 731 GCGCGCGCGGAGCTGTGCGCGCTGTCTCCCGAGCGCTGTGTGTCTCCGTGAGGTGTC 790
DB 142 GCGCGCGCGGAGCTGTGCGCGCTGTCTCTCCCGAGCGCTGTGTGTCTCCGAGAGGTGTC 83
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